


```
DE LILRB4 protein (Fragment).
GN Name=LILRB4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR542048; CAG46845.1; -
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR PROSITE; PS00835; IG-LIKE; 2.
FT NON TER 447
SQ SEQUENCE 447 AA; 49227 MW; 5DF5A3445A3AD4FF CRC64;

Query Match 27.9%; Score 499; DB 2; Length 447;
Best Local Similarity 36.0%; Pred. No. 1.6e-28;
Matches 133; Conservative 41; Mismatches 127; Indels 68; Gaps 9;

QY 1 MSPTALFCLGLG-RVPAQSGPLPKPSLQALPSSLVPLEKPTVLRQCGPPGVLDLYRL 59
Db 1 MIPTTALLCLGLSLGPRTHMQAGPLPKPTLWAEPSVISWGNSTVINCQGTLEAREYRL 60

QY 60 EKLSSRYQD-----QAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLVLATGV 110
Db 61 DKEESPAPWDRQNPLEPKPKARFIPSMTEYAGRYRCSYRSPVQWSQPSDPLELVMTGA 120

QY 111 FAKPSLSAQPAPVSSGGDVTLCQTRYGFDQFALYKEGDPAPY-----KNPERYRAS 165
Db 121 YSKPTLSALPSPLVTSKSVTLCCQSRSPMDTFLLIKERAHPLHLRSEHGAQHQAEF 180

QY 166 PIITVTAHSGTYRCYSFSSRDPLYWSAPSDPLELVVGTSTVTPSRPLTPEPPSSVAEF 225
Db 181 PMSPTSVHGGTYRCYFSSHGFHYLLSHPSDPLELVSGSLEDPRPSPT----- 229

QY 226 ATAELTVSFTNKVFTTSTSRITTSRKESDSDPAGPARQYTKG-----NLVRICLGA 279
Db 230 -----RSVSTAAGPEDQPLMPTGSPVPHSGLRHWEVLIGLVVVSIL 270

QY 280 LILLAGF-LAEDWHSRRKR-LRHGRVAVQRPPLPPLPQTRKSHGGQDGRQ----- 330
Db 271 LLSLLFLLLQHWROGKHRTLAQROADFQRPFGAARPEP-----KDGGLQRSSPAA 322

QY 331 DVHSRGLCS 339
Db 323 DVQGENFECA 331

RESULT 5
LIB4_HUMAN
ID LIB4_HUMAN STANDARD; PRT; 448 AA.
AC Q8NHJ6; O15468; O75021; Q8N1C7; Q8NHL5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leukocyte immunoglobulin-like receptor subfamily B member 4 precursor
DE (Leukocyte immunoglobulin-like receptor 5) (LIR-5) (Immunoglobulin-
DE like transcript 3) (ILT-3) (Monocyte inhibitory receptor HM18) (CD85k
DE antigen).
GN Name=LILRB4; Synonyms=ILT3, LIR5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Monocytes;
RX MEDLINE=97422556; PubMed=9278324;
RA Arm J.P., Nwankwo C., Austen K.F.;

RT RT Molecular identification of a novel family of human Ig superfamily
RT members that possess immunoreceptor tyrosine-based inhibition motifs
RT and homology to the mouse gp49B1 inhibitory receptor."
RL J. Immunol. 159:2342-2349(1997).
RN [2]
RC SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Peripheral blood leukocytes;
RX MEDLINE=98208234; PubMed=9548455;
RA Borges L., Hsu M.-L., Fanger N., Kubin M., Cosman D.;
RT "A family of human lymphoid and myeloid Ig-like receptors, some of
RT which bind to MHC class I molecules."
RL J. Immunol. 159:5192-5196(1997).
RN [3]
RC SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT GLU-362.
RX MEDLINE=20395285; PubMed=10941837; DOI=10.1007/s002510000183;
RA Liu W.R., Kim J., Nwankwo C., Ashworth L.K., Arm J.P.;
RT "Genomic organization of the human leukocyte immunoglobulin-like
RT receptors within the leukocyte receptor complex on chromosome
RT 19q13.4."
RL Immunogenetics 51:659-669(2000).
RN [4]
RC SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANT ASP-223.
RX Canavez F.C.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL [5]
RC SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RC FUNCTION, INTERACTION WITH PTPN6, PHOSPHORYLATION, TISSUE SPECIFICITY,
RC AND SUBCELLULAR LOCATION.
RX MEDLINE=97296504; PubMed=9151699;
RA Cella M., Doehring C., Samaridis J., Dessing M., Brockhaus M.,
RA Lanzavecchia A., Colonna M.;
RT "A novel inhibitory receptor (ILT3) expressed on monocytes,
RT macrophages, and dendritic cells involved in antigen processing."
RL J. Exp. Med. 185:1743-1751(1997).
RN [7]
RC FUNCTION.
RX MEDLINE=21864601; PubMed=11875462; DOI=10.1038/nr760;
RA Chang C.C., Ciubotariu R., Manavalan J.S., Yuan J., Colovai A.I.,
RA Piazza F., Lederman S., Colonna M., Cortesini R., Dalia-Favera R.,
RA Suciu-Foca N.;
RT "Tolerization of dendritic cells by T(S) cells: the crucial role of
RT inhibitory receptors ILT3 and ILT4."
RL Nat. Immunol. 3:237-243(2002).
CC -I- FUNCTION: Receptor for class I MHC antigens. Recognizes a broad
CC spectrum of HLA-A, HLA-B, HLA-C and HLA-G alleles. Involved in the
CC down-regulation of the immune response and the development of
CC tolerance, e.g. towards transplants. Interferes with TNFRSF5-
CC signaling and NF-kappa-B upregulation. Inhibits receptor-mediated
CC phosphorylation of cellular proteins and mobilization of
CC intracellular calcium ions.
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QY 60 EKLSSRYQD-----QAVLFIIPAMKRSIAGRYCSYQNGSLWSPDQLELVATGV 110
Db 61 YKEGSRPRDTQMPKPKARFSPMTHEHAGRYCYRSPAGWSEPSDLELVVTGF 120
QY 111 FAKPSLSAQPGPAVSSGGDVTLCQTRYGDFQFALYKEG----- 149
Db 121 YSTPTLSALPSPVAVSGNVTLRCGSKGYDFVLMKEGHEQLPQTLDSQHLHSGGFQAL 180
QY 150 -----DP-----AP----- 153
Db 181 FVPGVPTPSHRWTFTCYSYRNTPQVWSPDLEILPSGVSRKPSLLTLQGPVLAPGES 240
QY 154 -----YKNPER----- 159
Db 241 LTLQCGSDVGYDRFTLYKEGERDFLQLPQPQAGLSQANFTLGPVSRSHGGQYRCYGAH 300
QY 160 -----W----- 160
Db 301 NLSSEWAPSPLNLIAGQFYDRVSLSLQDPFTVASGENVTLLCQSQGFDTFLLTKEG 360
QY 161 -----YRASFPIITVTAHSGYRCYSFSSRDPLYMSAPSDLELVVTG 204
Db 361 AAHPPLRLRSKYQSKYQAEFPMNPVTSAAHAGTYRCYGSYSSPHLLSFPSDPLKLMVSG 420
QY 205 TSVTPSRLPTEPSSVAEFSEAFVLTFTVFTTETSRITSPKESDSPAGPARQY 264
Db 421 PSGSPSLPTGPPS-----TPASHAKD- 442
QY 265 YTKGNLVRLICLGAVALIILAGFLAEDWHSRR 295
Db 443 YTVENLIRMGMAGLVLVVLGILLFEAQHSQR 473
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RESULT 7
NCT1_RAT NCT1_RAT STANDARD; PRT; 325 AA.
AC Q9Z0H5;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Natural cytotoxicity triggering receptor 1 precursor (Natural killer cell p46-related protein) (NKp46) (NK-p46) (Rat activating receptor 1) (RAR-1) (Lymphocyte antigen 94 homolog) (NK receptor KILR-1) (NKACTR).
GN Name=Ncr1; Synonyms=Ar1, Klr1, Ly94;
OS Rattus norvegicus (Rat).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Lymphoid;
RX PubMed=10424451; DOI=10.1016/S0165-2478(99)00052-8;
RA Falco M., Cantoni C., Bottino C., Moretta A., Biassoni R.;
RT "Identification of the rat homologue of the human NKp46 triggering receptor."
RL Immunol. Lett. 68:411-414(1999).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=PVG;
RA Berg S.F., Dissen E., Westgaard I.H., Fossum S.;
RT "Molecular characterization of KILR-1, a novel immunoglobulin-like gene in the rat, expressed by NK cells."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Cytotoxicity activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis (By similarity).
CC -1- SUBUNIT: Interacts with CD32 and FCER1G (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Weakly expressed in spleen, heart and lung.
CC -1- SIMILARITY: Belongs to the natural cytotoxicity receptor (NCR) family.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like domains.
```

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CC -----
DR EMBL; AJ012741; CAA10161.1; -.
DR EMBL; AF082533; AAC69890.1; -.
DR HSSP; Q8NHL6; 1GOX.
DR RGD; 621288; Ly94.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; FALSE NEG.
KW Glycoprotein; Immunoglobulin domain; Receptor; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 16 Potential.
FT CHAIN 17 325 Natural cytotoxicity triggering receptor 1.
FT DOMAIN 17 258 Extracellular (Potential).
FT TRANSMEM 259 279 Potential.
FT DOMAIN 280 325 Cytoplasmic (Potential).
FT DOMAIN 42 100 Ig-like 1.
FT DOMAIN 137 192 Ig-like 2.
FT DISULFID 49 98 Potential.
FT DISULFID 144 190 By similarity.
FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 216 216 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 325 AA; 37178 MW; 502C10AA02F65FA4 CRC64;
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Query Match 26.3%; Score 469; DB 1; Length 325;
Best Local Similarity 37.7%; Pred. No. 1.7e-26;
Matches 116; Conservative 38; Mismatches 116; Indels 38; Gaps 5;

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QY 1 MSPSPTALFCLGCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYR- 58
Db 1 MLPTLTALLCLGCLSORINTKQTLPKPIIWAQPSIMVTGKNSVNIWCQGAQSASEYQL 60
QY 59 -----LEKLSSRYQDQAVLFIIPAMKRSIAGRYCSYQNGSLWSPDQLELVATGV 110
Db 61 YFEGSFFALERPKSSRMNKVKFFISQMTSHTAGIYTCFYQSGELWSESSNPLKLVVTGL 120
QY 111 FAKPSLSAQPGPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPWRWYRASFPIITV 170
Db 121 YDPTLWVHPGPEVTLGENVTFSCHLKTATSKFFLLKERESNHIQHKYGNIAQEPMPGV 180
QY 171 TAAHSGTYRCYCSFSSRDPLYMSAPSDLELVVTGTSVTPSRLPTEPPSSVA--EFSEATA 228
Db 181 TRAHRTYRC--FGSYNDYANFSPSEPVTLLITGEVENTSLAPDTPVSSLDYWEFLST- 237
QY 229 ELTVSFTNKVFTTETSRITSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLA 288
Db 238 -----KESGLQKDSAFWDHTAQNLIRIGLACIIVMALVWLLA 274
QY 289 EDWHSRRK 296
Db 275 EDWLSRRK 282
```

RESULT 8
Q8MJZ3
ID Q8MJZ3 PRELIMINARY; PRT; 631 AA.
AC Q8MJZ3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Leukocyte immunoglobulin-like receptor d.
GN Name=LIRd;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Db 121 YSKPTLSALPSPVVTSGGNTVLCQGSQALAFGGFTLCKEGED--EHPQCVNSQSHTLGS 177
162 RASFPIITVTAHSGTYRCYSFSSRDPYLSAPSDDPLELVVTGTSTVPSRLPTEPPSSVA 221
178 WAIFSVPVPSRRWSYRCYGDWSSPYVWSLPSGLLELLVPGVSKPS-LSVQPGPVVA 236
Qy 222 EFSEATAEL--TVSFTNKKVFTTETSRISITSPKESDSPAGPARQYTKGNLVRI----- 273
Db 237 PGEILTLQCSDDVGYDRFVLYKEGERDFLQLPGRQPQ-AGLSQANFTLGPVSRSHGGQYR 295
Qy 274 CLGA 277
Db 296 CCGA 299
RESULT 12
LIB3_HUMAN
ID LIB3_HUMAN STANDARD; PRT; 631 AA.
AC O75022; O15471; Q86U49;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leukocyte immunoglobulin-like receptor subfamily B member 3 precursor
DE (Leukocyte immunoglobulin-like receptor 3) (LIR-3) (Immunoglobulin-
DE like transcript 5) (ILT-5) (Monocyte inhibitory receptor HL9) (CD85a
DE antigen).
GN Name=LILRB3; Synonyms=ILTS, LIR3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANTS ARG-59; GLU-90; ASN-122;
RP GLN-205; HIS-405; PHE-409; GLN-539 AND VAL-574.
RC TISSUE=Monocytes;
RX MEDLINE=97422556; PubMed=9278324;
RA Arm J.P., Nwankwo C., Austen K.F.;
RT "Molecular identification of a novel family of human Ig superfamily
RT members that possess immunoreceptor tyrosine-based inhibition motifs
RT and homology to the mouse gp49BI inhibitory receptor.";
RL J. Immunol. 159:2342-2349 (1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), VARIANT ARG-400, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Peripheral blood leukocytes;
RX MEDLINE=98208234; PubMed=9548455;
RA Borges L., Hsu M.-L., Fanger N., Kubin M., Cosman D.;
RT "A family of human lymphoid and myeloid Ig-like receptors, some of
RT which bind to MHC class I molecules.";
RL J. Immunol. 159:5192-5196 (1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANTS GLU-90; GLN-205; HIS-405;
RP ARG-400; GLN-539 AND VAL-574.
RA Cuillerier B., Bahram S.;
RT "Genomics and diversity of the immunoglobulin-like transcript 5
RT locus.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May act as receptor for class I MHC antigens.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O75022-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O75022-2; Sequence=VSP_008459;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Detected in monocytes and B-cells.
CC -!- DOMAIN: Contains 3 copies of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC This motif is involved in modulation of cellular responses. The
CC phosphorylated ITIM motif can bind the SH2 domain of several SH2-
CC containing phosphatases.

CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; U91928; AAB6668.1; --
DR EMBL; AF025533; AAB87667.1; --
DR EMBL; AF256195; AAP30716.1; --
DR HSSP; Q8NHL6; IGOX.
DR Genew; HGNC:6607; LILRB3.
DR MIM; 604820; --
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Alternative splicing; Antigen; Glycoprotein; Immune response;
KW Immunoglobulin domain; Multigene family; Phosphorylation;
KW Polymorphism; Receptor; Repeat; Signal; Transmembrane.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 631 Leukocyte immunoglobulin-like receptor
FT subfamily B member 3.
FT DOMAIN 24 443 Extracellular (Potential).
FT TRANSMEM 444 464 Potential.
FT DOMAIN 465 631 Cytoplasmic (Potential).
FT DOMAIN 42 100 Ig-like C2-type 1.
FT DOMAIN 111 229 Ig-like C2-type 2.
FT DOMAIN 225 314 Ig-like C2-type 3.
FT DOMAIN 338 419 Ig-like C2-type 4.
FT SITE 512 517 ITIM motif 1.
FT SITE 593 598 ITIM motif 2.
FT SITE 623 628 ITIM motif 3.
FT DISULFID 49 98 By similarity.
FT DISULFID 144 196 By similarity.
FT DISULFID 245 296 Potential.
FT DISULFID 345 396 Potential.
FT CARBOHYD 139 139 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 280 280 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 301 301 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 340 340 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 437 437 G -> GGPEQPLNPPGSGPQNG (in isoform 2).
FT VARIANT 21 21 V -> M (in dbSNP:3745418).
FT VARIANT 59 59 Q -> R (in dbSNP:678876).
FT VARIANT 69 69 L -> W (in dbSNP:620207).
FT VARIANT 90 90 /FTId=VAR_017003.
FT VARIANT 122 122 Q -> E (in dbSNP:1052963).
FT VARIANT 122 122 S -> N (in dbSNP:3826750).
FT VARIANT 205 205 R -> Q (in dbSNP:1063805).
FT VARIANT 400 400 /FTId=VAR_017006.
FT VARIANT 400 400 Y -> R.
FT VARIANT 400 400 /FTId=VAR_017007.
FT VARIANT 400 400 Y -> H (in dbSNP:1052992).
FT VARIANT 400 400 /FTId=VAR_017008.
FT VARIANT 400 400 Y -> F (in dbSNP:8105096).
FT VARIANT 405 405 /FTId=VAR_017009.
FT VARIANT 405 405 Y -> H (in dbSNP:1132604).
FT VARIANT 409 409 /FTId=VAR_017010.
FT VARIANT 409 409 H -> F (in dbSNP:3193485).
FT VARIANT 539 539 /FTId=VAR_017011.
FT VARIANT 574 574 H -> Q (in dbSNP:1053002).
FT VARIANT 574 574 /FTId=VAR_017012.
FT VARIANT 574 574 A -> V (in dbSNP:1053008).
FT /FTId=VAR_017013.


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FT CONFLICT 53 53 L -> Q (in Ref. 3).
FT CONFLICT 61 61 D -> H (in Ref. 3).
FT CONFLICT 115 115 L -> M (in Ref. 3).
FT CONFLICT 120 120 A -> F (in Ref. 1).
FT CONFLICT 149 149 R -> G (in Ref. 1 and 3).
FT CONFLICT 175 175 G -> R (in Ref. 3).
FT CONFLICT 201 201 M -> T (in Ref. 3).
FT CONFLICT 252 252 D -> N (in Ref. 3).
FT CONFLICT 263 263 D -> A (in Ref. 3).
FT CONFLICT 268 268 P -> S (in Ref. 3).
FT CONFLICT 290 290 N -> H (in Ref. 1).
FT CONFLICT 417 417 V -> M (in Ref. 1).
FT CONFLICT 525 525 G -> R (in Ref. 1 and 3).
FT CONFLICT 561 561 P -> S (in Ref. 1 and 3).
SQ SEQUENCE 631 AA; 69233 MW; CC84A1762FC022DD CRC64;

Query Match 25.1%; Score 448; DB 1; Length 631;
Best Local Similarity 26.4%; Pred. No. 1.3e-24;
Matches 129; Conservative 45; Mismatches 87; Indels 228; Gaps 10;

Qy 1 MSPSPALFCLGCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLVRL 59
Db 1 MTPALTALLCLGSLGPRTRVQAGPPKPTLWAEPSVISWGSPVTIWCQGSLEAQEYQL 60

Qy 60 EKLSSSRYQD-----QAVLFIPAMKRSILAGRYCSYQNGSLWSLPSDQLELVATGV 110
Db 61 DKEGSPEPLDRNNPLEPKNKARFSIPMTQHHAGRYRCHYSSAGWSEPSDPLELVMTGA 120

Qy 111 FAKPSLSAQPGPAVSSGGDVTLCQ--QTRY----- 138
Db 121 YSKPTLSALPSPVVASGNNWTLRCGSQKRYHHFVLMKEGSHQLPRTLDSQQLHSGGFQAL 180

Qy 139 ----- 138
Db 181 FPGVPNPSHRWRFTCYYYVMNTPRVMSHPSPDPLEILPSGYSRKPSLLTLQGPVLAPGQS 240

Qy 139 -----GFDQFALYKEGD---PAPYKNPE----- 158
Db 241 LTLQCGSDVGYDRFVLYKEGERDFLQRPQGQPQAGLSQANFTLGPVSPNGGQYRCYGAH 300

Qy 159 ----RW----- 160
Db 301 NLSSEWSAPSDPLNILMAGQIYDVTLSLAQPGPTVASGENVTLLCQSWQFDTFLLTKEG 360

Qy 161 -----YRASFPPIITVTAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTG 204
Db 361 AAHPPLRLRSMYGAKHYQAEFPMPSPVTSAHAGTYRCYGSYSSNPYLLSHSPSEPLELVVSG 420

Qy 205 TSVTPSRLPTEPPSS--VAHFSEATAELTVSFTNKVF-----TTETSRISITSPKES 254
Db 421 HSGGSSLPPTGPPSTPGLGRYLEVLIGVSAFVLLLFLLFLLRRQRHSHKHRTSDQRKT 480

Qy 255 D--SPAGPA 261
Db 481 DFQRPAGAA 489
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RESULT 13
Q8MIZ8
ID Q8MIZ8 PRELIMINARY; PRT; 306 AA.
AC Q8MIZ8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NKp46vl.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA LaBonte M.L., Miller J., Letvin N.L.;
```

```
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY035219; AAK63121.1; -.
DR HSSP; O76036; 1OLL.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
SQ SEQUENCE 306 AA; 34650 MW; 0106E4D3DB465B21 CRC64;

Query Match 24.8%; Score 443.5; DB 2; Length 306;
Best Local Similarity 35.6%; Pred. No. 1.2e-24;
Matches 114; Conservative 40; Mismatches 119; Indels 47; Gaps 6;

Qy 1 MSPSPALFCLGCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLVRL 59
Db 1 MSSTLRALLCLGCLQSQRISAPKQTLPKPIRAESTYMPKPKQATLCCQGSYGAVEYQL 60

Qy 60 -----EKLSSSRYQDQAVLFIPAMKRSILAGRYCSYQNGSLWSLPSDQLE 104
Db 61 HFEGSLFAVERPKPPERINGVKFH-----IPMNSRKAGRYSCIYRVGELWRSERDILLD 114

Qy 105 LVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGFDQFALYKEGDPAPYKNPERWYRAS 164
Db 115 LVVTEMVDPTTLSVHPGPEVTSGEKVTFYCRLDTATSMFLLLKEGRSDRVQRSYKQVAE 174

Qy 165 FPIITVTAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFS 224
Db 175 FPMGPVTTAHRGSYRC--FGSYNNYAWSFPSEPVLKLVGTGDIENSTSLAPTD----- 224

Qy 225 EATAELTVSFTNKVFTTETSRISITTSPEKSDSPAGPARQYVTKGNLVRICLGAVILIILA 284
Db 225 -----TFPNSWDTCLLTR-----ETGLQKDLALWDHTAQNLLRMGLAFLVLVALV 269

Qy 285 GFLAEDWHSSRRKRLRHRGRA 304
Db 270 CLLVEDWLSRKRTREQASRA 289

RESULT 14
Q8MIZ9
ID Q8MIZ9 PRELIMINARY; PRT; 307 AA.
AC Q8MIZ9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE NKp46.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA LaBonte M.L., Miller J., Letvin N.L.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY035218; AAK63120.1; -.
DR HSSP; O76036; 1OLL.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
SQ SEQUENCE 307 AA; 34752 MW; DA1B8A36D2F9A751 CRC64;

Query Match 24.8%; Score 443; DB 2; Length 307;
Best Local Similarity 35.9%; Pred. No. 1.3e-24;
Matches 115; Conservative 40; Mismatches 119; Indels 46; Gaps 7;

Qy 1 MSPSPALFCLGCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLVRL 59
Db 1 MSSTLRALLCLGCLQSQRISAPKQTLPKPIRAESTYMPKPKQATLCCQGSYGAVEYQL 60

Qy 60 -----EKLSSSRYQDQAVLFIPAMKRSILAGRYCSYQNGSLWSLPSDQLE 104
Db 61 HFEGSLFAVERPKPPERINGVKFH-----IPMNSRKAGRYSCIYRVGELWRSERDILLD 114
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Db 61 HFEGLFAVERPKPPERINGVKFH-----IPDMNSRKAGRYSCIYRVGELMSERSDLLD 114

Qy 105 LVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKNPERWVRAS 164

Db 115 LVVTEMDTPTLSVHPGPEVTSGEKVTFYCRDLDTATSMFLLKKEGRSDVQRSYKGVQAE 174

Qy 165 FPIITVTAHSGTYRCYSFSSRDPYLSAPSDPLELVVTGTSVTPSRLETPPPSSVAEFS 224

Db 175 FPMGPVTTAHRGSYRC--FGSYNNYAWSPFSEPVKLLVTDGIENTSLAPDTPFP----- 227

Qy 225 EATAELTVSFTNKNKFTTTSRSTTSPPKESDSPAGPARQYVTKGNLVRLICLGAVILIILA 284

Db 228 -----TDSWDTCLLTRETG-----LQKDL-----ALWDHTAQNLLRMGLAFLVLVALV 270

Qy 285 GFLAEDWHSRRKRLRHRGRA 304

Db 271 CLLVEDWLSRKRTREQASRA 290

RESULT 15

LIA4 HUMAN

ID_LIA4_HUMAN STANDARD; PRT; 499 AA.

AC P59901;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Leukocyte immunoglobulin-like receptor subfamily A member 4 precursor (Immunoglobulin-like transcript 7) (ILT-7) (CD85g antigen).

GN Name=LILRA4; Synonyms=ILT7;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Colonna M.;

RT "Immunoglobulin-like transcript 7.";

RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 35-494 FROM N.A.

RA Canavez F.C.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP FUNCTION, AND TISSUE SPECIFICITY.

RX MEDLINE=22457157; PubMed=12529506; DOI=10.1073/pnas.0337567100;

RA Tedla N., Bandeira-Melo C., Tassinari P., Sloane D.E., Samplaski M.,

RA Cosman D., Borges L., Weller P.F., Arm J.P.;

RT "Activation of human eosinophils through leukocyte immunoglobulin-like receptor 7.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:1174-1179(2003).

CC -!- FUNCTION: May act as receptor for class I MHC antigens. Ligand binding leads to the activation of eosinophils and to the release of RNASE2, IL4 and leukotriene C4.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: Detected on eosinophils, neutrophils and monocytes.

CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF041261; AAD02203.1; -.

DR EMBL; AF283398; AAL36993.1; -.

DR MIM; 607517; -.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; ig; 4.

DR SMART; SM00409; IG; 3.

DR PROSITE; PS50835; IG_LIKE; 4.

KW Antigen; Glycoprotein; Immune response; Immunoglobulin domain;

KW Multigene family; Receptor; Repeat; Signal; Transmembrane.

FT SIGNAL 1 23 Potential.

FT CHAIN 24 499 Leukocyte immunoglobulin-like receptor subfamily A member 4.

FT DOMAIN 24 446 Extracellular (Potential).

FT TRANSMEM 447 467 Potential.

FT DOMAIN 468 499 Cytoplasmic (Potential).

FT DOMAIN 24 118 Ig-like C2-type 1.

FT DOMAIN 123 213 Ig-like C2-type 2.

FT DOMAIN 224 313 Ig-like C2-type 3.

FT DOMAIN 324 413 Ig-like C2-type 4.

FT DISULFID 49 98 By similarity.

FT DISULFID 143 195 By similarity.

FT DISULFID 244 295 Potential.

FT DISULFID 344 395 Potential.

FT CARBOHYD 138 138 N-linked (GlcNAc..)(Potential).

FT CARBOHYD 239 239 N-linked (GlcNAc..)(Potential).

FT CARBOHYD 279 279 N-linked (GlcNAc..)(Potential).

FT CARBOHYD 300 300 N-linked (GlcNAc..)(Potential).

FT CONFLICT 398 398 T -> S (in Ref. 2).

SQ SEQUENCE 499 AA; 55096 MW; 387DA38D45183676 CRC64;

Query Match 24.8%; Score 442.5; DB 1; Length 499;

Best Local Similarity 26.6%; Pred. No. 2.6e-24;

Matches 126; Conservative 57; Mismatches 111; Indels 179; Gaps 9;

Qy 1 MSPPTALFCLGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPTLRCQPPGVLDLYRL 59

Db 1 MTPILTVLICLGLSGPRTRVQAEENLPKPIIWAEPGVITWHPNPTIWCQGTLEAQGYRL 60

Qy 60 EK-----LSSRYQDQAVLFIPAMKRSLAGRYRCYQNGSLWSPDQLELVATGV 110

Db 61 DKEGMSRHLKLTLESENKVKLSIPSMMEHAGRYHCYQSPAGWSEPSDPLELVVT-A 119

Qy 111 FAKPSLSAQGPAPVSSGGDVTLQCQTRYGFDQFALYKEGDP-----PYKNPERWVRAS 164

Db 120 YSRPTLSALPSPVVTSGVNVTLRCASRLGLGRFTLIEGDHRLSWTLNSHONHGKFAQ 179

Qy 165 FPIITVTAHSGTYRCYSFSSRDPYLSAPSDPLELVVTGTSVTPSRL----- 212

Db 180 FPMGPLTFSNRGTFRCYGYENNTPYVWSEPSDPLQLLVSGVSRKPSLLTLQGPVVTGEN 239

Qy 213 ----- 212

Db 240 LTLQCGSDVGYIRYTLYKEGADGLPQRPGRQPQAGLSQANFTLSPVRSYGGQYRCYGAH 299

Qy 213 -----PTEP-----PS-SV----- 220

Db 300 NVSSEWSPSDPLDILIAGQISDRPSLSVQPGPTVTSGEKVTLLCQSWDPMFTLLTKEG 359

Qy 221 -----AEFSEATAELTVSFTNKFVTTETS----- 244

Db 360 AAHPPLRLRSMYGAHKYQAEFFMSPVTSAHAGTYRCYGTGTSNPNYLLSHSPSEPLELVSG 419

Qy 245 --RSITTSPEKESDSPAGPARQYVTKGNLVRLICLGAVILIILAAGFLAEDWHSRR 295

Db 420 ATETLNPAQKKSCKTAPHLDQDYTVENLRMGVAGLVLLFLGILLFEAQHSQR 472

Search completed: October 29, 2005, 02:56:15

Job time : 178 secs

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QY 61 KLSRRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
Db 61 KLSRRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
QY 181 YSFSSRDPYLWSPDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPYLWSPDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITSPKESDSPAGPARQYTKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITSPKESDSPAGPARQYTKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db 301 RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339

RESULT 2
US-09-829-495-3
; Sequence 3, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-3

Query Match 100.0%; Score 1786; DB 11; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.4e-128;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPSPTALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
Db 1 MSPSPTALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
QY 61 KLSRRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
Db 61 KLSRRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
QY 181 YSFSSRDPYLWSPDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPYLWSPDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITSPKESDSPAGPARQYTKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300

Db 241 TETSRITSPKESDSPAGPARQYTKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db 301 RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
RESULT 3
US-10-157-031-387
; Sequence 387, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 387
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-387

Query Match 100.0%; Score 1786; DB 14; Length 339;
Best Local Similarity 100.0%; Pred. No. 2.4e-128;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSPSPTALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
Db 1 MSPSPTALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
QY 61 KLSRRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
Db 61 KLSRRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 180
QY 181 YSFSSRDPYLWSPDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPYLWSPDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITSPKESDSPAGPARQYTKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITSPKESDSPAGPARQYTKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
Db 301 RGRAVQRPPLPPLPQTRKSHGGQDGRQDVHSRGLCS 339
RESULT 4
US-10-850-034-3
; Sequence 3, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034

Db 181 YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRRLTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRSTITSPKESDSPAGPARQYTKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRSTITSPKESDSPAGPARQYTKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVQRPLPPLPPLPQTRKSHGGQDGGRODVHSRGLCS 339
Db 301 RGRAVQRPLPPLPPLPQTRKSHGGQDGGRODVHSRGLCS 339

RESULT 7
US-09-832-312-38
; Sequence 38, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-38

Query Match 99.8%; Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
Db 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
QY 61 KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
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Db 121 GPAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
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Db 181 YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRRLTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRSTITSPKESDSPAGPARQYTKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRSTITSPKESDSPAGPARQYTKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVQRPLPPLPPLPQTRKSHGGQDGGRODVHSRGLCS 339
Db 301 RGRAVQRPLPPLPPLPQTRKSHGGQDGGRODVHSRGLCS 339

RESULT 8
US-09-832-312-40
; Sequence 40, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.

; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-40
Query Match 99.8%; Score 1782; DB 9; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
Db 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLE 60
QY 61 KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
Db 121 GPAVSSGGDVTLLQCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
QY 181 YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRRLTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPYLWSVPSDPLELVVTGTSVTPSRRLTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRSTITSPKESDSPAGPARQYTKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRSTITSPKESDSPAGPARQYTKGNLVRIICLGAVILIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVQRPLPPLPPLPQTRKSHGGQDGGRODVHSRGLCS 339
Db 301 RGRAVQRPLPPLPPLPQTRKSHGGQDGGRODVHSRGLCS 339

RESULT 9
US-09-829-495-34
; Sequence 34, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villeva J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-34

Query Match          99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
QY 61 KLSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSPLSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSPLSDQLELVATGVFAKPSLSAQ 120
QY 121 GAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
Db 121 GAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
QY 181 YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGQDGGGRQDVHSRGLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGQDGGGRQDVHSRGLCS 339

RESULT 10
US-09-829-495-36
; Sequence 36, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-36

Query Match          99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
QY 61 KLSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSPLSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSPLSDQLELVATGVFAKPSLSAQ 120
QY 121 GAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
Db 121 GAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
QY 181 YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLAEDWHSRRKRLRH 300
Db 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVALIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVORPLPPLPQTRKSHGGQDGGGRQDVHSRGLCS 339
Db 301 RGRAVORPLPPLPQTRKSHGGQDGGGRQDVHSRGLCS 339

RESULT 11
US-09-829-495-38
; Sequence 38, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-38

Query Match          99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
Db 1 MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE 60
QY 61 KLSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSPLSDQLELVATGVFAKPSLSAQ 120
Db 61 KLSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSPLSDQLELVATGVFAKPSLSAQ 120
QY 121 GAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
Db 121 GAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
QY 181 YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db 181 YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
```

QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVILIIILAGFLAEDWHSRRKRLRH 300
Db |||||
241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVILIIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVQRPLPPLPQLPQTRKSHGGQDGGQDQVHSRGLCS 339
Db |||||
301 RGRAVQRPLPPLPQLPQTRKSHGGQDGGQDQVHSRGLCS 339

RESULT 12
US-09-829-495-40
; Sequence 40, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villeva J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-829-495-40
Query Match 99.8%; Score 1782; DB 11; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSPSPTALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLE 60
Db |||||
1 MSPSPTALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLE 60
QY 61 KLSSSRYPQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSPLSDQLELVATGVFAKPSLSAQ 120
Db |||||
61 KLSSSRYPQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSPLSDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
Db |||||
121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
QY 181 YSFSSRDPLYWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db |||||
181 YSFSSRDPLYWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVILIIILAGFLAEDWHSRRKRLRH 300
Db |||||
241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVILIIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVQRPLPPLPQLPQTRKSHGGQDGGQDQVHSRGLCS 339
Db |||||
301 RGRAVQRPLPPLPQLPQTRKSHGGQDGGQDQVHSRGLCS 339

RESULT 13
US-10-850-034-34
; Sequence 34, Application US/10850034

; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villeva J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-850-034-34
Query Match 99.8%; Score 1782; DB 16; Length 339;
Best Local Similarity 99.7%; Pred. No. 4.8e-128;
Matches 338; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MSPSPTALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLE 60
Db |||||
1 MSPSPTALFCLGLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLE 60
QY 61 KLSSSRYPQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSPLSDQLELVATGVFAKPSLSAQ 120
Db |||||
61 KLSSSRYPQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSPLSDQLELVATGVFAKPSLSAQ 120
QY 121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
Db |||||
121 GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 180
QY 181 YSFSSRDPLYWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
Db |||||
181 YSFSSRDPLYWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT 240
QY 241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVILIIILAGFLAEDWHSRRKRLRH 300
Db |||||
241 TETSRITTSPKESDSPAGPARQYTKGNLVRLICLGAVILIIILAGFLAEDWHSRRKRLRH 300
QY 301 RGRAVQRPLPPLPQLPQTRKSHGGQDGGQDQVHSRGLCS 339
Db |||||
301 RGRAVQRPLPPLPQLPQTRKSHGGQDGGQDQVHSRGLCS 339

RESULT 14
US-10-850-034-36
; Sequence 36, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villeva J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034

; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-850-034-36

Query Match		99.8%;	Score 1782;	DB 16;	Length 339;
Best Local Similarity		99.7%;	Pred. No. 4.8e-128;		
Matches 338;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE	60
Db	1	MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE	60
Qy	61	KLSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP	120
Db	61	KLSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP	120
Qy	121	GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC	180
Db	121	GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC	180
Qy	181	YSFSSRDPLYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT	240
Db	181	YSFSSRDPLYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT	240
Qy	241	TETSRITTSKPESDSPAGPARQYTYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH	300
Db	241	TETSRITTSKPESDSPAGPARQYTYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH	300
Qy	301	RGRAVQRPLPPLPPLPQTRKSHGGQDGGGRQDVHSGRLCS	339
Db	301	RGRAVQRPLPPLPPLPQTRKSHGGQDGGGRQDVHSGRLCS	339

RESULT 15
US-10-850-034-38
; Sequence 38, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villeva J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-850-034-38

Query Match		99.8%;	Score 1782;	DB 16;	Length 339;
Best Local Similarity		99.7%;	Pred. No. 4.8e-128;		
Matches 338;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE	60
Db	1	MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLE	60
Qy	61	KLSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP	120
Db	61	KLSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQP	120
Qy	121	GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC	180
Db	121	GPAVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC	180
Qy	181	YSFSSRDPLYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT	240
Db	181	YSFSSRDPLYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT	240
Qy	241	TETSRITTSKPESDSPAGPARQYTYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH	300
Db	241	TETSRITTSKPESDSPAGPARQYTYTKGNLVRIICLGAVILIIILAGFLAEDWHSRRKRLRH	300
Qy	301	RGRAVQRPLPPLPPLPQTRKSHGGQDGGGRQDVHSGRLCS	339
Db	301	RGRAVQRPLPPLPPLPQTRKSHGGQDGGGRQDVHSGRLCS	339

Search completed: October 29, 2005, 03:10:28
Job time : 169 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 02:47:38 ; Search time 39 Seconds
(without alignments)
836.346 Million cell updates/sec

Title: US-09-503-387-3
Perfect score: 1786
Sequence: 1 MSPSPTALFCLGLCLGRVPA.....KSHGGQDGGGRQDVHSGRLCS 339

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1786	100.0	339	2 JC7509	glycoprotein VI-1
2	428.5	24.0	466	2 JC5897	killer cell inhibi
3	426.5	23.9	264	2 I46020	FC gamma 2 recepto
4	392	21.9	287	2 JH0332	IgA (Fc) receptor,
5	372.5	20.9	841	2 JC5894	killer cell inhibi
6	365.5	20.5	635	2 JC5896	killer cell inhibi
7	358.5	20.1	239	2 G02630	Fc alphaRb - human
8	356.5	20.0	680	2 JC5895	killer cell inhibi
9	335	18.8	444	2 G01925	KIR (cl-11) NK rec
10	330	18.5	296	2 B53434	cell surface glyco
11	328	18.4	348	2 A56247	natural killer cel
12	327	18.3	444	2 G01924	KIR (cl-2) NK rece
13	323.5	18.1	341	2 I61725	natural killer ass
14	322	18.0	1327	2 T09402	immunoglobulin-lik
15	317.5	17.8	335	2 A53434	cell surface glyco
16	316	17.7	455	2 G01923	KIR (cl-5) NK rece
17	315	17.6	427	2 G02034	killer cell inhibi
18	289.5	16.2	303	2 A40807	membrane glycoprot
19	182	10.2	184	2 T46433	hypothetical prote
20	145	8.1	237	2 A42013	alpha-1-B-glycopro
21	142.5	7.0	474	1 OMHUIB	heparan sulfate pr
22	126.5	7.1	3707	2 S18252	FC-gamma RIIB-alp
23	124.5	7.0	267	2 I56110	FC gamma (IgG) rec
24	118.5	6.6	267	2 A35902	perlecan precursor
25	118	6.6	4391	2 A38096	microtubule-associ
26	116	6.5	2774	2 A43359	FC gamma (IgG) rec
27	115	6.4	283	1 FCM5G1	Bravo/Nr-CAM cell
28	114.5	6.4	1259	2 A43425	hypothetical prote
29	113.5	6.4	592	2 D70863	

neural cell adhesi
dutt1 protein - mo
Fc-gamma receptor
connectin/titin -
IgE Fc receptor al
Fc gamma (IgG) rec
hypothetical prote
Fc gamma (IgG) rec
vascular cell adhe
related to glucan
long chain fatty a
Fc gamma (IgG) rec
Fc-gamma-1/gamma-2
Fc gamma receptor
transmembrane rece
glucan 1,4-alpha-g

30 113.5 6.4 1268 1 A39640
31 110.5 6.2 1612 2 T30805
32 110 6.2 270 2 A34636
33 109.5 6.1 4162 2 T42633
34 108 6.0 257 2 S00682
35 107 6.0 261 2 S29360
36 106.5 6.0 3375 2 T19821
37 106 5.9 285 2 S36903
38 106 5.9 739 2 JN0581
39 106 5.9 931 2 T49710
40 106 5.9 1607 2 T02837
41 105.5 5.9 330 2 A40071
42 105.5 5.9 330 2 I49660
43 104.5 5.9 267 2 I72882
44 104.5 5.9 1651 2 T14160
45 104 5.8 1367 1 S48478

ALIGNMENTS

RESULT 1
JC7509
glycoprotein VI-1 - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7509; PC7101
R;Ezumi, Y.; Uchiyama, T.; Takayama, H.
Biochem. Biophys. Res. Commun. 277, 27-36, 2000
A;Title: Molecular cloning, genomic structure, chromosomal localization, and alternative
A;Reference number: JC7509; MUID:20483673; PMID:11027634
A;Contents: Platelet
A;Accession: JC7509
A;Molecule type: mRNA
A;Residues: 1-339 <E2U>
A;Cross-references: UNIPROT:Q9UIF2; DDBJ:AB043819
A;Accession: PC7101
A;Molecule type: protein
A;Residues: 28-41;62-79;114-142 <E22>
C;Comment: This protein, which belongs to the immunoglobulin superfamily, is the major c
or gamma chain as a signal transducing subunit, and plays some roles in cancer cells.
C;Genetics:
A;Gene: gpVI-1
A;Map position: 19q13.4
A;Introns: 62/1; 95/1; 353/1; 638/1; 692/1; 752/1; 803/1
C;Keywords: glycoprotein; immunoglobulin; platelet

Query Match 100.0%; Score 1786; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 5.8e-122;
Matches 339; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPTALFCLGLCLGRVPAQSGDLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLE 60
|||||
Db 1 MSPTALFCLGLCLGRVPAQSGDLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLE 60
|||||

QY 61 KLSRRYQDQAVLPIPAKRSLAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP 120
|||||

Db 61 KLSRRYQDQAVLPIPAKRSLAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP 120
|||||

QY 121 GPVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFIITVTAHSGTYRC 180
|||||

Db 121 GPVSSGGDVTLCQTRYGDFQFALYKEGDPAPYKNPERWYRASFIITVTAHSGTYRC 180
|||||

QY 181 YFSRRDPYLWSAPSDPLELVVTGTSVTPSRPLTEPPSSVAEFSEATAELTVSFTNKVFT 240
|||||

Db 181 YFSRRDPYLWSAPSDPLELVVTGTSVTPSRPLTEPPSSVAEFSEATAELTVSFTNKVFT 240
|||||

QY 241 TETRSITTSKESDSPAGPARQYTKGNLVRLICGAVILIILAGFLAEDWHSRRKRLRH 300
|||||

Db 241 TETRSITTSKESDSPAGPARQYTKGNLVRLICGAVILIILAGFLAEDWHSRRKRLRH 300
|||||

QY 301 RGRAVQRPLPLPQTRKSHGGQDGGGRQDVHSGRLCS 339
|||||

Db 301 RGRAVQRLPPLPQTRKSHGGQDGRQDVHSGGLCS 339

RESULT 2
JC5897
killer cell inhibitory receptor p91 precursor - human
C:Species: Homo sapiens (man)
C>Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999
C:Accession: JC5897
R;Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohya
J. Biochem. 123, 358-368, 1998
A>Title: Genomic structures and chromosomal location of p91, a novel murine regulatory r
A:Reference number: JC5894; MUID:98218758; PMID:9538215
A:Accession: JC5897
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-466 <YMA>
A:Cross-references: GB:AF041034; NID:G2791689; PIDN:AAB96926.1; PID:G2791690
C:Comment: This protein function as inhibitory cell-surface molecule against cell activa
C:Genetics:
F;1-23/Domain: signal sequence #status predicted <SIG>

Query Match 24.0%; Score 428.5; DB 2; Length 466;
Best Local Similarity 36.1%; Pred. No. 1.4e-23;
Matches 126; Conservative 43; Mismatches 127; Indels 53; Gaps 13;

Qy 1 MSPSPATLFCGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVD---L 56
Db 1 MTPILTVLICLGLSLGPRTHVQAGHLPKPTLWAEPSGVIIQGSPTVTLRCQGLQAEYHL 60

Qy 57 YRLEKLSS--SRYQD---QAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVF 111
Db 61 YRENKSASVWRRIQEPGKNGQFPPIPSITWEHAGRYHCQYYSHNHSSEYSDPLELVVTGAY 120

Qy 112 AKPSLSAQPGPAVSSGGDVTLQCQTRYGFQDFALYKEGDPAPYKNPERW-----VR 162
Db 121 SKPTLSALPSPVVTGLGNVTLCQVSAFDFGLCKEGED---EHPQLNSHSHARGSSR 177

Qy 163 ASFPPIITVTAHSGTYRCYSFSSRDPLYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAE 222
Db 178 AIFSVGPVSPNRRWHRQYDNLSPYVWSSPDLLELLVPGVSKKPS-LSVQPGPVVAP 236

Qy 223 FSEATAELT--VSFTNKVFTTSTSRITTSKESDSPAGPARQYTYTKGNLVRI-----C 274
Db 237 GESLTQCQVSDVGYDRFVLYKEGERDLRQLPGRQPQ-AGLSQANFTLGPVSRSYGGQYRC 295

Qy 275 LGAVILIILAGFLAEDWHSRRKRLRHRGRAVQRPLPPLPQTRKSHG 323
Db 296 YGAY-----NLSSEWSA-----PSDPLDIL-ITGQIHG 322

RESULT 3
I46020
FC gamma 2 receptor precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I46020; S53115
R;Zhang, G.; Young, J.R.; Tregaskes, C.A.; Sopp, P.; Howard, C.J.
J. Immunol. 155, 1534-1541, 1995
A>Title: Identification of a novel class of mammalian Fc gamma receptor.
A:Reference number: I46020; MUID:95363119; PMID:7636215
A:Accession: I46020
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-264 <ZHA>
A:Cross-references: UNIPROT:Q28109; EMBL:Z37506; NID:G732571; PIDN:CAA85736.1; PID:G7325
C;Keywords: immunoglobulin receptor

Query Match 23.9%; Score 426.5; DB 2; Length 264;
Best Local Similarity 32.5%; Pred. No. 1e-23;
Matches 112; Conservative 37; Mismatches 87; Indels 109; Gaps 8;

Qy 1 MSPSPATLFCGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRL 59
Db 1 MAPTLFALLCLGLSVGLRTQVAGTFPKPIIWAEPSSVPLGSSVTLICQGGPPNTKSFSL 60

Qy 60 EKLSSS-----RYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATG- 109
Db 61 NKEGSDTPWNIHPSLEPDKANFFISNVREQAAGRYHCHSHFIVGNWSEFSEPLDLLVAGE 120

Qy 110 -----VFAKPSLSAQPGPAVSSGGDVTLQCQTRYGFQDFALYKEG---DPAPYKNPER-- 159
Db 121 EPAGRLDRPSSLVSRPSPVAPGENVTLLCQSGNRTDTFLLSKEGAHRPLRLRSQDQDG 180

Qy 160 WYRASPIITVTAHSGTYRCYSFSSRDPLYLWSAPSDPLELVVTGTSVTPSRLPTEPPSS 219
Db 181 WYQAEFSLSPVTSAHGGTYRCYRSLSTNPFYLLSQSPSEPLALLVAD----- 225

Qy 220 VAEFSEATAELTVSFTNKVFTTSTSRITTSKESDSPAGPARQYTYTKGNLVRIICLGA VI 279
Db 226 -----YTMQNLRMGLAASV 240

Qy 280 LIILAGFLAEDWHSRRKRLRHRGRAVQRPLPPLPQTRKSHGG 324
Db 241 LLLL-GIL-----LCQARHDHGG 257

RESULT 4
JH0332
IgA (Fc) receptor, myeloid cell (CD89) precursor - human
N:Alternate names: myeloid glycoprotein CD89
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JH0332; I37224; S14405
R;Maliszewski, C.R.; March, C.J.; Schoenborn, M.A.; Gimpel, S.; Shen, L.
J. Exp. Med. 172, 1665-1672, 1990
A>Title: Expression cloning of a human Fc receptor for IgA.
A:Reference number: JH0332; MUID:91079769; PMID:2258698
A:Accession: JH0332
A:Molecule type: mRNA
A:Residues: 1-287 <MAL>
A:Cross-references: UNIPROT:P24071; GB:X54150; NID:G31329; PIDN:CAA38089.1; PID:G31330
A:Experimental source: myeloid cell liver V937
R;de Wit, T.P.; Morton, H.C.; Capel, P.J.; van de Winkel, J.G.
J. Immunol. 155, 1203-1209, 1995
A>Title: Structure of the gene for the human myeloid IgA Fc receptor (CD89).
A:Reference number: I37224; MUID:95363085; PMID:7636188
A:Accession: I37224
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-287 <RES>
A:Cross-references: EMBL:X87767; NID:G963041; PIDN:CAA61039.1; PID:G1054737
C:Genetics:
A:Gene: GDB:FCAR; CD89
A:Cross-references: GDB:127543; OMIM:147045
A:Map position: 19q13.2-19q13.4
A:Introns: 12/1; 24/1; 121/1; 217/1
C:Keywords: Glycoprotein; immunoglobulin receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-287/Product: IgA receptor Fc alpha #status predicted <MFC>
F;228-246/Domain: transmembrane #status predicted <TRA>
F;65,79,141,177,186/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.9%; Score 392; DB 2; Length 287;
Best Local Similarity 31.2%; Pred. No. 3.5e-21;
Matches 100; Conservative 43; Mismatches 110; Indels 68; Gaps 5;

Qy 1 MSPSPATLFCGLCLG-RVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRL 59
Db 1 MDPKQTTLLCLVLCGLQRIQAQEGDFMPFISAKSSPVIPLDGSVKIQCOAIREAYLTQL 60

Qy 60 EKLSSSRYQD-----QAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVAT 108
Db 61 MIKNSTYREIGRRLKFWNETDPEFVIDHMDANKAGRYCQYRIGHYFRFRISDTLELVVT 120

A;Title: Genomic structures and chromosomal location of p91, a novel murine regulatory p
A;Reference number: JC5894; MUID:98218758; PMID:9538215
A;Accession: JC5895
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-680 <YAM>
A;Cross-references: UNIPROT:Q55001; GB:AF041035; NID:g2791691; PIDN:AAB96927.1; PID:g279
C;Comment: This protein function as inhibitory cell-surface molecule against cell activa
C;Genetics:
A;Map position: 7
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-118,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like #status p
F;636-674/Domain: transmembrane #status predicted <TM>
F;675-680/Domain: cytoplasmic #status predicted <CYT>

Query Match 20.0%; Score 356.5; DB 2; Length 680;
Best Local Similarity 22.9%; Pred. No. 3.6e-18;
Matches 106; Conservative 50; Mismatches 111; Indels 195; Gaps 7;

QY 22 SCGLPKPSLQALPSSSLVPLEKPVTLRCQPPGVDLYRLEKLSRSSRYQDAVL----- 73
Db 220 SGNLQKPTIKAEPGSVITSKRMTIWCQNLDAEVYFLHNEKSQKTQTTLQOPGNKGR 279

QY 74 -FIPAMKRSLAGRYCSYQNGSLWSLPSDQLELVATGVFA--KPSLSAQPGPAVSSGGDV 130
Db 280 FPIPSVTQOHAGQRCYCYSSAGWSQPSDTLELVVTGIYVNEPRLSLLPSVVRPGNM 339

QY 131 TLQCQTRYGDFQFALYKEG-----PAPYKNPERWYRASFPITVTAAHSGTYRCYSPS 184
Db 340 TLHCASQGHYDKFILTKEKFKFANALDTEHISSSRQYQALFIGPTTPTHTGTFRCYGY 399

QY 185 SRDPYLWSAPSDPLELVVTGTSTVPS----- 210
Db 400 KNTPLQWSVPSNLQQILISGLSKKPSLLTHQGHILDPGMTLTLCQCFSDMNYDRFALHKVG 459

QY 211 -----R 211
Db 460 GADIMQHSSQQTIDIGFSVANFTILGYVSSSTGGQYRCYGAHNLSSEWSASSEPLDLITGQ 519

QY 212 LPTEPPSSV-----AE 222
Db 520 LPLTPSLSVQPNHTVHSGETVSLLCWSMDSVDTFILSKEGSAQOPLRLKSKSHDQQSQAE 579

QY 223 FS-----EAPAEITVSFTNKVFTTETSRITTSRKES 254
Db 580 FMSAVTSHLSGTYRCYGAQDSFYLLSSASAPVELTVS-----GTIESSWPPKRP 631

QY 255 DSPAGPARQYTYKGNLVRICLGAVIDLIILAGFLAEDWHSRRK 296
Db 632 NPPIPTENQDHTMENLIRMGMAVVVFIVLSILATEAWRSRQ 673

RESULT 9
G01925
KIR (cl-11) NK receptor precursor protein - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G01925; I61726
R;Wagtmann, N.
submitted to the EMBL Data Library, June 1995
A;Reference number: G08782
A;Accession: G01925
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 1-444 <WAG>
A;Cross-references: UNIPROT:P43629; EMBL:U30274; NID:g1004360; PIDN:AAB52522.1; PID:g100
R;Colonna, M.; Samaridis, J.
Science 268, 405-408, 1995
A;Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B p
A;Reference number: A56247; MUID:95232526; PMID:7716543
A;Accession: I61726
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: mRNA

A;Residues: 1-444 <RES>
A;Cross-references: GB:L41269; NID:g780307; PIDN:AAAG9870.1; PID:g780308
C;Genetics:
A;Gene: NKAT-3
A;Map position: 19

Query Match 18.8%; Score 335; DB 2; Length 444;
Best Local Similarity 30.4%; Pred. No. 7.8e-17;
Matches 112; Conservative 34; Mismatches 127; Indels 96; Gaps 12;

QY 1 MSPSPALTFLCLGLGRVP-----AQSGPL-----PKPSLQALPSSSLVPLEKPV 45
Db 82 MSPVTTAHAGNYTCRGSHPHSPTGWSAPSNPWIMVTGNHRKPSLLAHPGLVKSGERVI 141
QY 46 LRCQGGPPGVDLRLEKLSRSSRYQDAV-----LFIPAMKRSLAGRYRC----- 88
Db 142 LQCWSDIMEHFHFLHKEGISKDPSRLVGOIHGVSKANFSGPMMLALAGTYRCYGSVTH 201
QY 89 -SYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTTLQCQTRYGDFQFALYK 147
Db 202 TPYQ----LSAPSDPLDIVVTGPYEKPSLSAQPGPKVQAGESVTLSCSSRSSYDMYHLSR 257
QY 148 EGDPAFYKNP-----ERWYRASFPITVTAAHSGTYRCYCSFSSRDPYLSWAPSDDPLELV 202
Db 258 EGGAHERRLPAVRKVNRTQADFPL--GPATHGGTYRCFCFSRHSFYENSDPSDLLVSV 315
QY 203 TGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSPKESDSPAGPAR 262
Db 316 TG-----NPSS-----WPSPTSPSSKSGNPR 337
QY 263 QYTYKGNLVRICLGAVIDLIILAGFLAEDWHSRRKRLRHRGRAVQRPLPPLPQTRKSH 322
Db 338 HLHI---LIGTSVVIILFILLFLLHLWCNNK-----NAAV-----MDQEPAGNR 383
QY 323 GGQDGGRRQD 331
Db 384 NSEDSDEQD 392

RESULT 10
B53434
cell surface glycoprotein gp49B form 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
C;Accession: B53434
R;Castells, M.C.; Wu, X.; Arm, J.P.; Austen, K.F.; Katz, H.R.
J. Biol. Chem. 269, 8393-8401, 1994
A;Title: Cloning of the gp49B gene of the immunoglobulin superfamily and demonstration th
A;Reference number: A53434; MUID:94179223; PMID:8132564
A;Accession: B53434
A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-296 <CAS>
A;Cross-references: UNIPROT:Q64281; GB:U05265; NID:g475446; PIDN:AAAL7798.1; PID:g475448;
C;Genetics:
A;Gene: gp49B
A;Introns: 12/3; 24/2; 119/2; 220/1; 232/1; 249/3; 272/1
C;Keywords: alternative splicing; glycoprotein

Query Match 18.5%; Score 330; DB 2; Length 296;
Best Local Similarity 36.1%; Pred. No. 1.1e-16;
Matches 88; Conservative 33; Mismatches 101; Indels 22; Gaps 6;

QY 6 TALFCLGLCL-GRVPAQSGPLPKPSLQALPSSSLVPLEKPVTLRCQPPGVDLYRLEKLS 64
Db 6 TVLLYLGLILEPRTAVQAGHLPKPIIWAEPGSIYAAYTSVITWCQGSWEAQYHYHLYKEKS 65
QY 65 SRYQD-----QAVLFIPAMKRSLAGRYRCYQNGSLWSLPSDQLELVATGVFAKPS 115
Db 66 VNPWDTQVPLETRNKAKFNIPSMTTTSYAGIYKCYYESAAGFSEHSDAMELVMTGAYENPS 125
QY 116 LSAQPGPAVSSGGDVTTLQCQTRYGDFQFALYKEG-----DPAPYKNPERWYRASFP 167

Db 126 LSVYPPSNVTSGVISFSCSSSIVFGRFILIOEGKHGLSWTLDSQHQANQPSY--ATFVL 183
QY 168 ITVTAHAHSGTYRCYCFSSRDPYLWAPSDDPLELVVGTSTVTPSRKLPTEPPSSVAEF-SEA 226
Db 184 DAVTPNHNGTFRCYGYFRNEPQVWSKPSNSLDLMISETK-DQSSPTEDDASVKNTQSEN 242
QY 227 TAEI 230
Db 243 NAEI 246

RESULT 11
A56247
natural killer cell-associated protein - human
C;Species: Homo sapiens (man)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: A56247
R;Colonna, M.; Samaridis, J.
Science 268, 405-408, 1995
A;Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B
A;Reference number: A56247; MUID:95232526; PMID:7716543
A;Accession: A56247
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-348 <RES>
A;Cross-references: UNIPROT:P43626; GB:L41267; NID:g780303; PIDN:AAA69868.1; PID:g780304
C;Genetics:
A;Gene: GDB:NKAT1
A;Cross-references: GDB:698165
A;Map position: 19

Query Match 18.4%; Score 328; DB 2; Length 348;
Best Local Similarity 31.0%; Pred. No. 1.9e-16;
Matches 101; Conservative 34; Mismatches 107; Indels 84; Gaps 11;
QY 1 MSPSPALFCLGLCL--GRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYR 58
Db 1 MSLVVMACVGFLLQGAWP-HEGVHRKPSLLAHPGLVKSEETVILQCWSVDVMEHFL 59
QY 59 LEKLSRRYQD-----QAVLFIPAMKRSLAGRYRC-----SYQNGSLWSL 98
Db 60 LHR--EGMFNDTLRLIGEHHGDSKANFISIRMTQDLAGTYRCYGSVTHSPYQ-----VSA 113
QY 99 PSDQLVLVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKNP- 157
Db 114 PSDPLDIVIIGLYEKPSLSAQPGPTVLAGENVTLSCSRSSSYDMYHLSREGEAHERRLPA 173
QY 158 ----ERWYRASFPITVTAAHSGTYRCYCFSSRDPYLWAPSDDPLELVVGTSTVTPSRLP 213
Db 174 GPKVNGTFOADFP--GPATHGGTYRCFGSHDPSYEWSSKSDPLLVSVTGNPSNSWSP 231
QY 214 TEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSPPKESDSPAGPARQYTTKGNLVRI 273
Db 232 TEPSSK-----TGPNRH-----LHI 246
QY 274 CLG---AVILIIILAGFLAEDWHSRRK 296
Db 247 LGTSTVVIILFILLFLLHRWCNNK 272

RESULT 12
G01924
KIR (cl-2) NK receptor precursor - human
N;Alternate names: killer cell inhibitory receptor
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C;Accession: G01924; G01945
R;Wagtmann, N.
submitted to the EMBL Data Library, June 1995
A;Reference number: G08780
A;Accession: G01924
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA

A;Residues: 1-444 <WAG>
A;Cross-references: EMBL:U30273; NID:g1004358; PIDN:AAB52521.1; PID:g1004359
R;D'Andrea, A.; Chang, C.; Franz-Bacon, K.; McLanahan, T.; Phillips, J.H.; Lanier, L.L.
submitted to the EMBL Data Library, July 1995
A;Reference number: G08908
A;Accession: G01945
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-444 <DXA>
A;Cross-references: EMBL:U31416; NID:g973405; PIDN:AAC23725.1; PID:g973406
C;Genetics:
A;Gene: NKB1

Query Match 18.3%; Score 327; DB 2; Length 444;
Best Local Similarity 30.1%; Pred. No. 2.9e-16;
Matches 111; Conservative 34; Mismatches 128; Indels 96; Gaps 12;
QY 1 MSPSPALFCLGLCLGRVP-----AQSGPL-----PKPSLQALPSSLVPLEKPV 45
Db 82 MSPVTTAHAGNVTCTGSHPHSPGWSAPSNPVVIMVTGNHRKPSLLAHPGLVKSGEVI 141
QY 46 LRCQGGPPGVDLYRLEKLSRRYQDQAV-----LFIPAMKRSLAGRYRC----- 88
Db 142 LQCWSDIMFEHFLHKEGISKDPSRLVQIHDGVSKANFSGPMMALAGTYRCYGSVTH 201
QY 89 -SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYGFDQFALYK 147
Db 202 TPYQ---LSAPSDPLDIVVTGPEYKPSLSAQPGPKVQAGESVTLSCSRSSSYDMYHLSR 257
QY 148 EGDPAKYKNP-----ERWYRASFPITVTAAHSGTYRCYCFSSRDPYLWAPSDDPLELVV 202
Db 258 ERGAHERRLPAVRKVNRTFOADFP--GPATHGGTYRCFGSFRHSPYEWSDPSDPLLVS 315
QY 203 TGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSPPKESDSPAGPAR 262
Db 316 TG-----NPSSS-----WPSPTSPSSKSGNPR 337
QY 263 QYTKGNLVRIICGAVILIIILAGFLAEDWHSRRKRLHRGRAVQRPPLPPLPQTRKSH 322
Db 338 HLHI---LIGTSVVIILFILLFLLHLWCNNK-----NAAV-----MDQEPAGNRTA 383
QY 323 GQDGGGRQD 331
Db 384 NSEDSDEQD 392

RESULT 13
I61725
natural killer associated transcript 2 - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I61725
R;Colonna, M.; Samaridis, J.
Science 268, 405-408, 1995
A;Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B
A;Reference number: A56247; MUID:95232526; PMID:7716543
A;Accession: I61725
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-341 <RES>
A;Cross-references: UNIPROT:P43628; GB:L41268; NID:g780305; PIDN:AAA69869.1; PID:g780306
C;Genetics:
A;Gene: NKAT-2

Query Match 18.1%; Score 323.5; DB 2; Length 341;
Best Local Similarity 30.1%; Pred. No. 3.9e-16;
Matches 99; Conservative 36; Mismatches 105; Indels 89; Gaps 12;
QY 1 MSPSPALFCLGLCL--GRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYR 58
Db 1 MSLMVVMVCMVGVFLLQGAWP-HEGVHRKPSLLAHPGLVKSEETVILQCWSVDVRFQHFL 59
QY 59 LEKLSRRYQD-----QAVLFIPAMKRSLAGRYRC-----SYQNGSLWSL 98

Db 60 LHR--EGKFKDTLHLIGEHHGVSKANFSIGPMQDLAGRYCYGSVTHSPYQ-----LSA 113
Qy 99 PSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGFDQFALYKGD-----P 151
Db 114 PSDPLDIVITGLYEKPSLSAQPGPTVLAGESVTLCSSRSSYDMYHLSRGEAHERRFA 173
Qy 152 APYKNPERWYRASFPPIITVTAHSGTYRCYFSFSSRDPYLSAPSDPLELVVTGTSVTPSR 211
Db 174 GPKVNGT--FQADFPL--GPATHGGTYRCFSGFRDSPYEWNSSDPLLVSVTGNPNSWP 229
Qy 212 LPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRISITTSKESDSPAGPARQYTKGNLV 271
Db 230 SPTEPSSE-----TGNPRH-----L 244
Qy 272 RICLGA-----VILIILAGFLAEDWHSRRK 296
Db 245 HVLIGTSVVILFILLFFLLHRWCCKK 273
RESULT 14
T09402
immunoglobulin-like protein IGSF1 - human
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09402
R:Mazzarella, R.; Pengue, G.; Jones, J.; Jones, C.; Schlessinger, D.
Genomics 48, 157-162, 1998
A:Title: Cloning and expression of an immunoglobulin superfamily gene (IGSF1) in Xq25.
A:Reference number: Z16665; MUID:98190514; PMID:9521868
A:Accession: T09402
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1327 <MAZ>
A:Cross-references: UNIPROT:O15070; EMBL:AF034198; NID:g2645889; PIDN:AAC52057.1; PID:g2645889
C:Genetics:
A:Gene: igsf1
A:Map position: Xq25
Query Match 18.0%; Score 322; DB 2; Length 1327;
Best Local Similarity 32.1%; Pred. No. 2.5e-15;
Matches 105; Conservative 37; Mismatches 133; Indels 52; Gaps 9;
Qy 26 PKPSLQALPSSLVPLEKPVTLRCQGP---PGVDLYRLEKLSRRY---QQAFLFIPAM 78
Db 960 PKPWLFAEPSSVVMGQNVTLWCRGPVHGVGYILHKEGATSMQLWGSTNSDGAFFITNI 1019
Qy 79 KRSLAGRYRCYQ---NGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQ 135
Db 1020 SGTSMGRYSCCYHPDWTSSIKIQPSNTLELVTLGLLPKPSLLAQPGPMVAPGENMTLQ 1079
Qy 136 TRYGFDQFALYKEG--DPAPYKNPERWYRASFPPIITVTAHSGTYRCYFSFSSRDPYLSA 193
Db 1080 GELPDSTFVLLKEGAQEPLEQORPS-GYRADFWMPAVRGEDSGDIYSCVYVLDSTPFAASN 1138
Qy 194 PSDPLELVVTGTSVTPS-----RLPTEPPSSVAEF-----SEATAELT- 231
Db 1139 HSDSLEIWIWTDKPPKPSLSANPSTMFKLGKDITLQCRGPLPGVEFVLEHGDGEAPQFSE 1198
Qy 232 -----VSFTNKVFTTETSRISITTSKESDSPAGPARQYTKGNLVRI 275
Db 1199 DGDFVINNVGKIGNYSCSYRLQAYPDIWSEPSDPLELVGAAGPAQECTVGNIVRSSL 1258
Qy 276 GAVILIILAGFLAEDWHSRRKRLRHG 302
Db 1259 IVVVVALGVVLAIEW-KKWPRLRTRG 1284

RESULT 15
A53434
cell surface glycoprotein gp49B form 1 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 09-Jul-2004

C:Accession: A53434
R:Castells, M.C.; Wu, X.; Arm, J.P.; Austen, K.F.; Katz, H.R.
J. Biol. Chem. 269, 8393-8401, 1994
A:Title: Cloning of the gp49B gene of the immunoglobulin superfamily and demonstration of
A:Reference number: A53434; MUID:94179223; PMID:8132564
A:Accession: A53434
A:Status: preliminary
A:Molecule type: DNA; mRNA
A:Residues: 1-335 <CAS>
A:Cross-references: UNIPROT:Q64281; GB:U05265; NID:g475446; PIDN:AAA17797.1; PID:g475447;
C:Genetics:
A:Gene: gp49B
A:Introns: 12/3; 24/2; 119/2; 220/1; 232/1; 271/1; 288/3; 311/1
C:Keywords: alternative splicing; glycoprotein

Query Match 17.8%; Score 317.5; DB 2; Length 335;
Best Local Similarity 34.0%; Pred. No. 1e-15;
Matches 84; Conservative 36; Mismatches 104; Indels 23; Gaps 6;

Qy 6 TALFCIGLCL-GRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVVDLYRLEKLS 64
Db 6 TVLLYLGLLEPRTAVQAGHLPKPIIWAEPGSVIAAYTSVITWCQGSWEAQYHYLYKEK 65
Qy 65 SRYQD-----QAVLFIPAMKRSLAGRYRCYQNGSLWSLPSDQLELVATGVFAKPS 115
Db 66 VNPWDTQVPLETRNKAKFNIPSMTTSYAGIYKCYESAAGFSEHSDAMELVMTGAYENPS 125
Qy 116 LSAQPGPAVSSGGDVTLCQTRYGFDQFALYKEG-----DPAPYKNPERWYRASFP 167
Db 126 LSVYPSSNVTSGVSI SFSCSSSIVFGRFILLIQEGKHGLSWTLDSQHQAQNP SY--ATFVL 183
Qy 168 ITVTAHSGTYRCYFSFSSRDPYLSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEAT 227
Db 184 DAVTPNHNGTFRCYGYFRNEPQVWSKPSNSLDLMISETK-DQSSTPTE--DGLETYQKIL 240
Qy 228 AELTVSF 234
Db 241 IGVLSVF 247

Search completed: October 29, 2005, 02:57:49
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 03:38:13 ; Search time 41 Seconds
(without alignments)
453.357 Million cell updates/sec

Title: US-09-503-387-3_COPY_21_269
Perfect score: 1304
Sequence: 1 QSGPLPKPSLQALPSSLVPL.....SPKESDPAGPARQYVTKGN 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 413575

Minimum DB seq length: 0
Maximum DB seq length: 250

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1304	100.0	249	3	US-09-345-468-9 Sequence 9, Appli
2	1304	100.0	249	3	US-09-414-453A-9 Sequence 9, Appli
3	268	20.6	47	3	US-09-345-468-7 Sequence 7, Appli
4	268	20.6	47	3	US-09-414-453A-7 Sequence 7, Appli
5	220	16.9	47	3	US-09-345-468-23 Sequence 23, Appli
6	220	16.9	47	3	US-09-414-453A-23 Sequence 23, Appli
7	216	16.6	41	3	US-09-345-468-6 Sequence 6, Appli
8	216	16.6	41	3	US-09-414-453A-6 Sequence 6, Appli
9	187	14.3	50	3	US-09-345-468-13 Sequence 13, Appli
10	187	14.3	50	3	US-09-414-453A-13 Sequence 13, Appli
11	164	12.6	41	3	US-09-345-468-22 Sequence 22, Appli
12	164	12.6	41	3	US-09-414-453A-22 Sequence 22, Appli
13	162.5	12.5	135	3	US-08-985-950-10 Sequence 10, Appli
14	162.5	12.5	135	4	US-09-546-049-10 Sequence 10, Appli
15	131	10.0	105	4	US-09-513-999C-4313 Sequence 4313, Ap
16	100	7.7	172	2	US-08-756-387B-13 Sequence 13, Appli
17	100	7.7	172	3	US-09-285-873-13 Sequence 13, Appli
18	100	7.7	172	4	US-09-245-764-9 Sequence 9, Appli
19	100	7.7	172	4	US-09-944-277A-13 Sequence 13, Appli
20	100	7.7	197	2	US-08-756-387B-11 Sequence 11, Appli
21	100	7.7	197	3	US-09-285-873-11 Sequence 11, Appli
22	100	7.7	197	4	US-09-944-277A-11 Sequence 11, Appli
23	100	7.7	232	1	US-07-869-933-13 Sequence 13, Appli
24	100	7.7	232	2	US-08-756-387B-6 Sequence 6, Appli
25	100	7.7	232	3	US-09-103-663-13 Sequence 13, Appli
26	100	7.7	232	3	US-09-285-873-6 Sequence 6, Appli
27	100	7.7	232	4	US-09-944-277A-6 Sequence 6, Appli

28	98	7.5	193	2	US-08-765-536-1	Sequence 1, Appli
29	98	7.5	193	5	PCT-US95-08401-1	Sequence 1, Appli
30	96.5	7.4	197	3	US-08-788-954-2	Sequence 2, Appli
31	94	7.2	201	3	US-09-015-734-12	Sequence 12, Appli
32	94	7.2	201	4	US-09-515-311-12	Sequence 12, Appli
33	94	7.2	238	2	US-08-768-964-7	Sequence 7, Appli
34	94	7.2	238	3	US-09-005-299-7	Sequence 7, Appli
35	94	7.2	238	3	US-09-515-431-7	Sequence 7, Appli
36	93	7.1	236	3	US-09-015-734-7	Sequence 7, Appli
37	93	7.1	236	4	US-09-515-311-7	Sequence 7, Appli
38	92	7.1	247	4	US-09-910-174B-31	Sequence 31, Appli
39	90	6.9	197	3	US-08-833-488B-4	Sequence 4, Appli
40	90	6.9	197	3	US-08-833-488B-9	Sequence 9, Appli
41	88	6.7	173	3	US-08-833-488B-31	Sequence 31, Appli
42	88	6.7	197	3	US-08-833-488B-28	Sequence 28, Appli
43	88	6.7	229	3	US-08-833-488B-24	Sequence 24, Appli
44	88	6.7	233	2	US-08-667-939A-7	Sequence 7, Appli
45	88	6.7	233	4	US-08-433-123-7	Sequence 7, Appli
46	87	6.7	199	3	US-08-833-488B-14	Sequence 14, Appli
47	86	6.6	233	2	US-08-667-939A-5	Sequence 5, Appli
48	86	6.6	233	4	US-08-433-123-5	Sequence 5, Appli
49	85	6.5	233	2	US-08-667-939A-8	Sequence 8, Appli
50	85	6.5	233	4	US-08-433-123-8	Sequence 8, Appli
51	84	6.4	215	2	US-08-667-939A-18	Sequence 18, Appli
52	84	6.4	215	4	US-08-433-123-18	Sequence 18, Appli
53	82	6.3	233	2	US-08-667-939A-6	Sequence 6, Appli
54	82	6.3	233	4	US-08-433-123-6	Sequence 6, Appli
55	81	6.2	174	2	US-08-768-964-13	Sequence 13, Appli
56	81	6.2	174	3	US-09-005-299-13	Sequence 13, Appli
57	81	6.2	174	3	US-09-515-431-13	Sequence 13, Appli
58	81	6.2	174	4	US-09-245-764-8	Sequence 8, Appli
59	81	6.2	199	2	US-08-768-964-12	Sequence 12, Appli
60	81	6.2	199	3	US-09-005-299-12	Sequence 12, Appli
61	81	6.2	199	3	US-09-515-431-12	Sequence 12, Appli
62	81	6.2	213	4	US-09-538-092-1255	Sequence 1255, Ap
63	80.5	6.2	203	2	US-08-667-939A-20	Sequence 20, Appli
64	80.5	6.2	203	4	US-08-433-123-20	Sequence 20, Appli
65	79.5	6.1	140	3	US-08-986-485-4	Sequence 4, Appli
66	79.5	6.1	169	4	US-09-489-039A-8371	Sequence 8371, Ap
67	78.5	6.0	235	3	US-09-423-439-58	Sequence 58, Appli
68	78.5	6.0	235	4	US-09-011-769A-23	Sequence 23, Appli
69	78	6.0	236	2	US-08-070-116A-2	Sequence 2, Appli
70	78	6.0	236	4	US-08-557-050-2	Sequence 2, Appli
71	78	6.0	246	1	US-08-469-486-57	Sequence 57, Appli
72	78	6.0	246	2	US-08-469-658-57	Sequence 57, Appli
73	77.5	5.9	222	2	US-08-190-199A-67	Sequence 67, Appli
74	77.5	5.9	235	2	US-08-303-569B-5	Sequence 5, Appli
75	77.5	5.9	235	2	US-08-116-247-5	Sequence 5, Appli
76	77.5	5.9	235	4	US-09-795-515-5	Sequence 5, Appli
77	77.5	5.9	235	4	US-09-348-224-5	Sequence 5, Appli
78	77	5.9	232	1	US-08-425-763-2	Sequence 2, Appli
79	77	5.9	232	3	US-08-811-757-2	Sequence 2, Appli
80	77	5.9	232	3	US-09-249-230-2	Sequence 2, Appli
81	75.5	5.8	132	4	US-09-252-991A-30729	Sequence 30729, A
82	75.5	5.8	159	2	US-08-653-402B-2	Sequence 2, Appli
83	75.5	5.8	207	3	US-08-652-877-13	Sequence 13, Appli
84	75.5	5.8	207	3	US-08-476-515A-13	Sequence 13, Appli
85	75.5	5.8	231	4	US-09-252-991A-17973	Sequence 17973, A
86	75.5	5.8	235	3	US-08-444-644-28	Sequence 28, Appli
87	75.5	5.8	235	3	US-08-232-246A-28	Sequence 28, Appli
88	75	5.8	231	1	US-08-168-091A-4	Sequence 4, Appli
89	75	5.8	241	1	US-07-847-743B-30	Sequence 30, Appli
90	75	5.8	241	1	US-08-456-201-30	Sequence 30, Appli
91	75	5.8	241	2	US-08-456-241-30	Sequence 30, Appli
92	75	5.8	241	5	PCT-US92-04295A-30	Sequence 30, Appli
93	74.5	5.7	204	4	US-09-562-737-127	Sequence 127, App
94	74.5	5.7	230	6	5169835-13	Patent No. 5169835
95	74.5	5.7	230	6	5169835-13	Patent No. 5169835
96	74	5.7	207	4	US-08-467-602-219	Sequence 219, App
97	74	5.7	207	4	US-08-411-295F-145	Sequence 145, App
98	74	5.7	210	4	US-08-467-602-215	Sequence 215, App
99	74	5.7	210	4	US-08-411-295F-141	Sequence 141, App
100	74	5.7	229	3	US-08-751-359-22	Sequence 22, Appli

ALIGNMENTS

RESULT 1
US-09-345-468-9
; Sequence 9, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-9

Query Match 100.0%; Score 1304; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 6.6e-121;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLVRLKLSSSRYQDQAVLFIPAMKR 60
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLVRLKLSSSRYQDQAVLFIPAMKR 60

QY 61 SLAGRYRCYQNGSLWLSPLSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGF 120
Db 61 SLAGRYRCYQNGSLWLSPLSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGF 120

QY 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYSFSSRDPYLWSAPSDPLEL 180
Db 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYSFSSRDPYLWSAPSDPLEL 180

QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSKPESDSPAGP 240
Db 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSKPESDSPAGP 240

QY 241 ARQYYTKGN 249
Db 241 ARQYYTKGN 249

RESULT 2
US-09-414-453A-9
; Sequence 9, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-9

Query Match 100.0%; Score 1304; DB 3; Length 249;
Best Local Similarity 100.0%; Pred. No. 6.6e-121;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLVRLKLSSSRYQDQAVLFIPAMKR 60
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLVRLKLSSSRYQDQAVLFIPAMKR 60

QY 61 SLAGRYRCYQNGSLWLSPLSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGF 120
Db 61 SLAGRYRCYQNGSLWLSPLSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGF 120

QY 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYSFSSRDPYLWSAPSDPLEL 180
Db 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYSFSSRDPYLWSAPSDPLEL 180

QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSKPESDSPAGP 240
Db 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSKPESDSPAGP 240

QY 241 ARQYYTKGN 249
Db 241 ARQYYTKGN 249

RESULT 3
US-09-345-468-7
; Sequence 7, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-7

Query Match 20.6%; Score 268; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 160
Db 1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRC 47

RESULT 4
US-09-414-453A-7
; Sequence 7, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0

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; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-7

Query Match      20.6%; Score 268; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 160
Db 1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 47

RESULT 5
US-09-345-468-23
; Sequence 23, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-345-468-23

Query Match      16.9%; Score 220; DB 3; Length 47;
Best Local Similarity 78.7%; Pred. No. 1e-14;
Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 160
Db 1 CQSPYSFDEFVLYKEGDTGPYKRPEKWRANFPPIITVTAHSGTYRC 47

RESULT 6
US-09-414-453A-23
; Sequence 23, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-414-453A-23

Query Match      16.9%; Score 220; DB 3; Length 47;
Best Local Similarity 78.7%; Pred. No. 1e-14;
Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 160
Db 1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 160

RESULT 9
US-09-345-468-13
; Sequence 13, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-6

Query Match      16.6%; Score 216; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CQPPGVDLYRLEKLSRSSRYQDQAVLFIPAMKRSLAGRYRC 68
Db 1 CQPPGVDLYRLEKLSRSSRYQDQAVLFIPAMKRSLAGRYRC 41
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; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-7

Query Match      20.6%; Score 268; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e-19;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 160
Db 1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 47

RESULT 5
US-09-345-468-23
; Sequence 23, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-6

Query Match      16.6%; Score 216; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CQPPGVDLYRLEKLSRSSRYQDQAVLFIPAMKRSLAGRYRC 68
Db 1 CQPPGVDLYRLEKLSRSSRYQDQAVLFIPAMKRSLAGRYRC 41

RESULT 8
US-09-414-453A-6
; Sequence 6, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-6

Query Match      16.6%; Score 216; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CQPPGVDLYRLEKLSRSSRYQDQAVLFIPAMKRSLAGRYRC 68
Db 1 CQPPGVDLYRLEKLSRSSRYQDQAVLFIPAMKRSLAGRYRC 41

RESULT 9
US-09-345-468-13
; Sequence 13, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-6

Query Match      16.6%; Score 216; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.1e-14;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 CQPPGVDLYRLEKLSRSSRYQDQAVLFIPAMKRSLAGRYRC 68
Db 1 CQPPGVDLYRLEKLSRSSRYQDQAVLFIPAMKRSLAGRYRC 41
```

; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-345-468-13

Query Match 14.3%; Score 187; DB 3; Length 50;
Best Local Similarity 74.5%; Pred. No. 2e-11;
Matches 35; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 24 VTLCQGPVVDLYRLEKLSRRYQDQAVLFIPAMKRSIAGRYRCSY 70
| ||||| ||||| :||| ||||| :||| |||||
Db 4 VILRCQGPVVDLYRLEKLPKPKYEDQDFLFIPTMERSNAGRYRCSY 50

RESULT 10
US-09-414-453A-13
; Sequence 13, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-414-453A-13

Query Match 14.3%; Score 187; DB 3; Length 50;
Best Local Similarity 74.5%; Pred. No. 2e-11;
Matches 35; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 24 VTLCQGPVVDLYRLEKLSRRYQDQAVLFIPAMKRSIAGRYRCSY 70
| ||||| ||||| :||| ||||| :||| |||||
Db 4 VILRCQGPVVDLYRLEKLPKPKYEDQDFLFIPTMERSNAGRYRCSY 50

RESULT 11
US-09-345-468-22
; Sequence 22, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 41
; TYPE: PRT

; ORGANISM: Mus musculus
US-09-345-468-22

Query Match 12.6%; Score 164; DB 3; Length 41;
Best Local Similarity 73.2%; Pred. No. 2.9e-09;
Matches 30; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 28 CQPPGVVDLYRLEKLSRRYQDQAVLFIPAMKRSIAGRYRRC 68
| ||||| ||||| :||| ||||| :||| |||||
Db 1 CQPPGVVDLYRLEKLPKPKYEDQDFLFIPTMERSNAGRYRRC 41

RESULT 12
US-09-414-453A-22
; Sequence 22, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-414-453A-22

Query Match 12.6%; Score 164; DB 3; Length 41;
Best Local Similarity 73.2%; Pred. No. 2.9e-09;
Matches 30; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 28 CQPPGVVDLYRLEKLSRRYQDQAVLFIPAMKRSIAGRYRRC 68
| ||||| ||||| :||| ||||| :||| |||||
Db 1 CQPPGVVDLYRLEKLPKPKYEDQDFLFIPTMERSNAGRYRRC 41

RESULT 13
US-08-985-950-10
; Sequence 10, Application US/08985950
; Patent No. 6140076
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/033,181


```

; FILING DATE: 16-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-985-950-10

Query Match 12.5%; Score 162.5; DB 3; Length 135;
Best Local Similarity 31.6%; Pred. No. 2.3e-08;
Matches 42; Conservative 15; Mismatches 43; Indels 33; Gaps 3;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSSSRYQD----- 49
Db 22 QEGALPRPSISAEPGTVISPGSHVTFMCRGPGVGVQTFRLEREDRAKYKDSYNVFRLLGPSE 81
QY 50 -QAVLFIPAMKRSLAGRYRCYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGG 108
Db 82 SEARFHIDSVSEGNAGLYRCLYKPPGWSHSDFLELLVKGTV-----PGTEAS--- 130
QY 109 DVTLCQCTRYGFD 121
Db 131 -----GFD 133

RESULT 14
US-09-546-049-10
; Sequence 10, Application US/09546049
; Patent No. 6479638
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
; Meyaard, Linde
; Gorman, Daniel M.
; McClanahan, Terrill K.
; Zurawski, Sandra M.
; Zurawski, Gerard
; Lanier, Lewis L.
; Phillips Jr., Joseph H.
; TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/546,049
; FILING DATE: 10-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,950
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: US 60/041,279
; FILING DATE: 21-MARCH-1997
; APPLICATION NUMBER: US 60/033,181

; FILING DATE: 16-DEC-1996
; APPLICATION NUMBER: US 60/032,252
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0670K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1204
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-546-049-10

Query Match 12.5%; Score 162.5; DB 4; Length 135;
Best Local Similarity 31.6%; Pred. No. 2.3e-08;
Matches 42; Conservative 15; Mismatches 43; Indels 33; Gaps 3;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSSSRYQD----- 49
Db 22 QEGALPRPSISAEPGTVISPGSHVTFMCRGPGVGVQTFRLEREDRAKYKDSYNVFRLLGPSE 81
QY 50 -QAVLFIPAMKRSLAGRYRCYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGG 108
Db 82 SEARFHIDSVSEGNAGLYRCLYKPPGWSHSDFLELLVKGTV-----PGTEAS--- 130
QY 109 DVTLCQCTRYGFD 121
Db 131 -----GFD 133

RESULT 15
US-09-513-999C-4313
; Sequence 4313, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4313
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -21...-1
; OTHER INFORMATION: score 9.5
; OTHER INFORMATION: seq LGLVLCLAQTIHT/QE
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 47
; OTHER INFORMATION: Xaa= * or Tyr
; US-09-513-999C-4313

Query Match 10.0%; Score 131; DB 4; Length 105;
Best Local Similarity 36.6%; Pred. No. 2.1e-05;
Matches 30; Conservative 11; Mismatches 29; Indels 12; Gaps 1;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSSSRYQD----- 49
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Db 22 QEEDLPRPSISAEPTVPLGSHVTFVCRGPGVQVTFRLERESRSTXNDTEDVSQASPSE 81
Qy 50 -QAVLFIPAMKRSLAGRYRCSY 70
Db 82 SEARFRIDSVSEGNAGPYRCIY 103

RESULT 16

US-08-756-387B-13
; Sequence 13, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-756-387B-13

Query Match 7.7%; Score 100; DB 2; Length 172;
Best Local Similarity 24.7%; Pred. No. 0.049;
Matches 47; Conservative 27; Mismatches 78; Indels 38; Gaps 9;
Qy 6 PKPSLQALPSSLVPLEKPVTLRCQGGVVDLYRLEKLSRSSRY-----QDQAVLFIPA 57
Db 5 PKVSLNP-PWNRIFKGENVTLCNG-----NNFEVSSTKWFHNGSLSEETNSSLNIVN 57
Qy 58 MKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTR 117
Db 58 AKFEDSGEYKCOHQ-----VNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGW 110
Qy 118 YGFDQFAL--YKEGDPAPYKNPERWY-RASFPITVTAAHSGTYRCYSFSSRDPYLWSA- 173
Db 111 RNWDVYKVIYKDGALKY-----WYENHNISITNATVEDSGTYCTG-----KVMQLD 159
Qy 174 -PSDPLELVV 182
Db 160 YESEPLNITV 169

RESULT 17

US-09-285-873-13
; Sequence 13, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-285-873-13

Query Match 7.7%; Score 100; DB 3; Length 172;
Best Local Similarity 24.7%; Pred. No. 0.049;
Matches 47; Conservative 27; Mismatches 78; Indels 38; Gaps 9;
Qy 6 PKPSLQALPSSLVPLEKPVTLRCQGGVVDLYRLEKLSRSSRY-----QDQAVLFIPA 57
Db 5 PKVSLNP-PWNRIFKGENVTLCNG-----NNFEVSSTKWFHNGSLSEETNSSLNIVN 57
Qy 58 MKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTR 117
Db 58 AKFEDSGEYKCOHQ-----VNESEPVYLEVFSDWLLQLQASAEVVMGQPLFLRCHGW 110
Qy 118 YGFDQFAL--YKEGDPAPYKNPERWY-RASFPITVTAAHSGTYRCYSFSSRDPYLWSA- 173
Db 111 RNWDVYKVIYKDGALKY-----WYENHNISITNATVEDSGTYCTG-----KVMQLD 159
Qy 174 -PSDPLELVV 182
Db 160 YESEPLNITV 169

RESULT 18

US-09-245-764-9
; Sequence 9, Application US/09245764
; Patent No. 6675105
; GENERAL INFORMATION:
; APPLICANT: Hogarth, P. Mark
; APPLICANT: Powell, Maree S.

Qy 6 PKPSLQALPSSSLVPLEKPVTLRCQPPGVLDYLRLEKLSRRY-----QDQAVLFIPA 57
Db 30 PKVSLNP-PWNRIFKGENVTLCNG-----NNFEVSSTKWFHNGSLSEETNSSLNIVN 82
Qy 58 MKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTR 117
Db 83 AKFEDSGEYKCHQHQ-----VNESEPVYLEVFSDWLLQASAEVVMGQPLFLRCHGW 135
Qy 118 YGFDQFAL--YKGGDPAPYKNPERWY-RASFPITVTAHSGTYRCYSFSSRDPYLWSA- 173
Db 136 RNWDVYKVIYKDGALKY-----WYENHNISITNATVEDSGTYCTG-----KMWQLD 184
Qy 174 -PSDPLELVV 182
Db 185 YESEPLNITV 194

RESULT 23
US-07-869-933-13
; Sequence 13, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; TITLE OF INVENTION: IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapien
; STRAIN: FCRI alpha subunit
; US-07-869-933-13

Query Match 7.7%; Score 100; DB 1; Length 232;
Best Local Similarity 24.7%; Pred. No. 0.075;
Matches 47; Conservative 27; Mismatches 78; Indels 38; Gaps 9;
Qy 6 PKPSLQALPSSSLVPLEKPVTLRCQPPGVLDYLRLEKLSRRY-----QDQAVLFIPA 57
Db 5 PKVSLNP-PWNRIFKGENVTLCNG-----NNFEVSSTKWFHNGSLSEETNSSLNIVN 57
Qy 58 MKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTR 117
Db 58 AKFEDSGEYKCHQHQ-----VNESEPVYLEVFSDWLLQASAEVVMGQPLFLRCHGW 110

Qy 118 YGFDQFAL--YKGGDPAPYKNPERWY-RASFPITVTAHSGTYRCYSFSSRDPYLWSA- 173
Db 111 RNWDVYKVIYKDGALKY-----WYENHNISITNATVEDSGTYCTG-----KMWQLD 159
Qy 174 -PSDPLELVV 182
Db 160 YESEPLNITV 169

RESULT 24
US-08-756-387B-6
; Sequence 6, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-756-387B-6

Query Match 7.7%; Score 100; DB 2; Length 232;
Best Local Similarity 24.7%; Pred. No. 0.075;
Matches 47; Conservative 27; Mismatches 78; Indels 38; Gaps 9;
Qy 6 PKPSLQALPSSSLVPLEKPVTLRCQPPGVLDYLRLEKLSRRY-----QDQAVLFIPA 57
Db 5 PKVSLNP-PWNRIFKGENVTLCNG-----NNFEVSSTKWFHNGSLSEETNSSLNIVN 57
Qy 58 MKRSLAGRYRCSYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTR 117
Db 58 AKFEDSGEYKCHQHQ-----VNESEPVYLEVFSDWLLQASAEVVMGQPLFLRCHGW 110
Qy 118 YGFDQFAL--YKGGDPAPYKNPERWY-RASFPITVTAHSGTYRCYSFSSRDPYLWSA- 173
Db 111 RNWDVYKVIYKDGALKY-----WYENHNISITNATVEDSGTYCTG-----KMWQLD 159
Qy 174 -PSDPLELVV 182
Db 160 YESEPLNITV 169

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OM protein - protein search, using sw model

Run on: October 29, 2005, 03:33:47 ; Search time 167 Seconds
(without alignments)
576.667 Million cell updates/sec

Title: US-09-503-387-3_COPY_21_269
Perfect score: 1304
Sequence: 1 QSGPLPKPSLQALPSSLVPL.....SPKESDSPAGPARQYVTKGN 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1541488

Minimum DB seq length: 0
Maximum DB seq length: 250

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	1304	100.0	249	4	AAB61261 Human TAN
2	1304	100.0	249	6	ABU11227 Human TAN
3	970	74.4	203	5	AAO19266 Human pla
4	378.5	29.0	236	5	AAO19236 Human LIR
5	355.5	27.3	237	5	AAE19107 Human NKp
6	300	23.0	227	8	ADO24405 Human PRO
7	279.5	21.4	170	4	ABG10157 Novel hum
8	275.5	21.1	205	5	AAO19235 Human imm
9	272	20.9	74	4	AAO19235 Human imm
10	272	20.9	74	4	AAO19235 Human pla
11	268	20.6	47	4	AAO19235 Human TAN
12	268	20.6	47	6	ABU11225 Human TAN
13	245	18.8	228	5	AAO19233 Human FcR
14	233	17.9	145	5	AAO19233 Human put
15	227.5	17.4	100	4	ABB42669 Peptide #
16	227.5	17.4	100	4	AAO19233 Peptide #
17	227.5	17.4	100	4	AAO19233 Protein #
18	227.5	17.4	100	4	AAO19233 Human bon
19	227.5	17.4	100	4	AAO19233 Human bra
20	227.5	17.4	100	4	ABG58080 Human liv
21	227.5	17.4	100	4	ABG45662 Human pep
22	220	16.9	47	4	AAO19233 Mouse TAN
23	220	16.9	47	6	ABU11238 TANGO 268
24	218.5	16.8	221	8	ADK98546 Human imm
25	216.5	16.6	100	4	AAM15998 Peptide #

99	154	11.8	115	2	AAW78263	Aaw78263 Fragment
100	154	11.8	120	2	AAW78154	Aaw78154 Human sec
ALIGNMENTS						
RESULT 1						
AAB61261						
ID	AAB61261 standard; protein; 249 AA.					
XX						
AC	AAB61261;					
XX						
DT	04-APR-2001 (first entry)					
XX						
DE	Human TANGO 268 extracellular domain.					
XX						
KW	Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;					
KW	thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;					
KW	platelet membrane glycoprotein receptor; bleeding disorder;					
KW	blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;					
KW	ischaemia; cardiovascular disease; immunological disease; liver disorder;					
KW	cancer.					
XX						
OS	Homo sapiens.					
XX						
PN	WO200100810-A1.					
XX						
PD	04-JAN-2001.					
XX						
PF	30-JUN-2000; 2000WO-US018152.					
XX						
PR	30-JUN-1999; 99US-00345468.					
PR	06-DEC-1999; 99US-00454824.					
PR	14-FEB-2000; 2000US-00503387.					
XX						
PA	(MILL-) MILLENNIUM PHARM INC.					
XX						
PI	Busfield SJ, Villelal J, Jandrot-Perrus M, Vainchencker W;					
PI	Gill DS, Qian MD, Kingsbury G;					
XX						
DR	WPI; 2001-080877/09.					
XX						
PT	New genes encoding human platelet-expressed collagen receptor,					
PT	glycoprotein VI, and its modulators, useful for preventing, treating and					
PT	diagnosing hemorrhagic disorders, thrombotic diseases and immunological					
PT	disorders.					
XX						
PS	Disclosure; Page 203-204; 227pp; English.					
XX						
CC	The present sequence is given in a specification relating to an isolated					
CC	nucleic acid molecule encoding a platelet membrane glycoprotein receptor					
CC	glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides					
CC	and polypeptides and their modulators, e.g. antisense nucleic acids,					
CC	ribozymes and antibodies, are useful for preventing, treating and					
CC	diagnosing disorders associated with aberrant expression or activity of					
CC	GPVI. These disorders include bleeding disorders (e.g.					
CC	thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.					
CC	thrombotic occlusion of the coronary arteries), haemorrhagic disorders,					
CC	coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),					
CC	cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),					
CC	immunological diseases (e.g. platelet disorder) and embryonic liver					
CC	disorders. Preferably they are used to prevent acture cardiac ischaemia					
CC	following angioplasty and metastatic cancers, especially of the colon and					
CC	liver					
XX						
SQ	Sequence 249 AA;					
Query Match 100.0%; Score 1304; DB 4; Length 249;						
Best Local Similarity 100.0%; Pred. NO. 5.5e-105;						
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
OY	1 QSGPLPKPSIQALPSSLVPLEKXPVTLRCQGPQVDVLRLEKLSRRYQDQAVLFIPAMKR 60					

Db	1	QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSRRYQDQAVLFIPAMKR	60
QY	61	SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGF	120
Db	61	SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGF	120
QY	121	DQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRCYSFSSRDPYLWSAPSDPLEL	180
Db	121	DQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRCYSFSSRDPYLWSAPSDPLEL	180
QY	181	VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRSITTSPEKESDSPAGP	240
Db	181	VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRSITTSPEKESDSPAGP	240
QY	241	ARQYYTKGN 249	
Db	241	ARQYYTKGN 249	
RESULT 2			
ABU11227			
ID	ABU11227 standard; peptide; 249 AA.		
XX			
AC	ABU11227;		
XX			
DT	06-FEB-2003 (first entry)		
XX			
DE	Human TANGO 268 extracellular domain.		
XX			
KW	Human; mouse; variable heavy; VH; antigen; cancer;		
KW	complementarity determining region; TANGO 268; glycoprotein VI; GPVI;		
KW	TANGO 268; extracellular matrix; collagen; platelet release;		
KW	proliferation; migration; embryogenesis; inflammation; thrombosis;		
KW	degranulation; thrombocytopaenia; antibody; thrombotic disorder;		
KW	cerebral vascular disease; stroke; ischaemia; venous thromboembolism;		
KW	leg swelling; pain; ulceration; pulmonary embolism; coronary disease;		
KW	cardiovascular disease; angina pectoris; myocardial infarction;		
KW	coronary restenosis; atherosclerosis; immunological disorder;		
KW	developmental disorder; embryonic disorder; liver disorder;		
KW	cerebral vascular disease; venous thromboembolism disease.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200280968-A1.		
XX			
PD	17-OCT-2002.		
XX			
PF	09-APR-2002; 2002WO-US011122.		
XX			
PR	09-APR-2001; 2001US-00829495.		
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Busfield SJ, Villeval J, Jandrot-Perrus M, Vainchencker W;		
PI	Gill DS, Qian DM, Kingsbury G;		
XX			
DR	WPI; 2003-058477/05.		
XX			
PT	Novel substantially purified antibody immunospecifically binding to TANGO		
PT	268 antigen, useful for treating bleeding disorders such as		
PT	thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.		
XX			
PS	Disclosure; Page 212-213; 236pp; English.		
XX			
CC	This invention relates to a novel purified antibody comprising a variable		
CC	heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;		
CC	or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically		
CC	binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.		
CC	The antibodies of the invention act to decrease or block TANGO 268		
CC	binding to extracellular matrix components, or as a Collagen or platelet		
CC	release and aggregation blocker. The antibodies of the invention are		
CC	useful for modulating proliferation, migration, morphology,		

CC differentiation and/or function of megakaryocytes and platelets,
CC including during development e.g. embryogenesis, modulating leukocyte-
CC platelet and platelet-endothelium interactions in inflammation and/or
CC thrombosis, and modulating platelet aggregation and degranulation. They
CC are also useful for modulating disorders associated with abnormal or
CC aberrant megakaryocyte and/or platelet proliferation, migration,
CC morphology, differentiation and/or function, e.g. bleeding disorders such
CC as thrombocytopenia. Other diseases which may be modulated by these
CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
CC coronary diseases (e.g. cardiovascular diseases including angina
CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
CC etc); immunological disorders, developmental disorders, embryonic
CC disorders, liver disorders, cerebral vascular diseases, venous
CC thromboembolism disease, coronary diseases, and metastatic cancers. The
CC antibodies of the invention only causes a transient decrease in platelet
CC counts, platelet aggregation, and/or platelet activation and so have some
CC advantages over prior art methods. The present sequence represents a
CC peptide sequence used to generate the antibodies of the invention
XX
SQ Sequence 249 AA;

Query Match 100.0%; Score 1304; DB 6; Length 249;
Best Local Similarity 100.0%; Pred. No. 5.5e-105;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRSSRYQDQAVLFIPAMKR 60
DB 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRSSRYQDQAVLFIPAMKR 60
QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120
DB 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120
QY 121 DQFALYKEGDPAPYKKNPERWYRASFPITVTTAAHSGTYRCYFSRSSRDPYLSAPSDPLEL 180
DB 121 DQFALYKEGDPAPYKKNPERWYRASFPITVTTAAHSGTYRCYFSRSSRDPYLSAPSDPLEL 180
QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTTSRITTSRKESDSPAGP 240
DB 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTTSRITTSRKESDSPAGP 240
QY 241 ARQYYTKGN 249
DB 241 ARQYYTKGN 249

RESULT 3
AAO19266
ID AAO19266 standard; protein; 203 AA.

XX AAO19266;
XX
DT 27-NOV-2002 (first entry)
XX
DE Human platelet glycoprotein VI-2 protein SEQ ID NO: 75.
XX
KW Human; leukocyte immunoglobulin receptor-like protein; LIR-like protein;
KW vulnary; neuroprotective; anti-inflammatory; cerebroprotective;
KW nutritional supplement; lymphoid disorder; burn; wound; ulcer; stroke;
KW Alzheimer's disease; amyotrophic lateral sclerosis; fibrosis; cancer;
KW immune disorder; multiple sclerosis; allergy; inflammation; infertility;
KW cytostatic; immunosuppressive; anti-diabetic; antiinfertility.
XX
OS Homo sapiens.
XX
PN WO200266600-A2.
XX
PD 29-AUG-2002.
XX
PF 28-DEC-2001; 2001WO-US049435.
XX

PR 29-DEC-2000; 2000US-00751518.
XX (HYSE-) HYSEQ INC.
XX
PI Boyle BJ, Kuo C, Mize NK, Haley-Vicente DA, Arterburn MC;
PI Tang YT, Zhou P, Liu C, Asundi V, Drmanac RT, Yeung G, Palencia S;
XX WPI; 2002-674924/72.
XX
XX New leukocyte immunoglobulin receptor-like (LIR-like) polynucleotides and
PT polypeptides, useful in research, as nutritional sources, or for treating
PT wounds, Alzheimer's disease, inflammations, infertility, stroke or
PT cancers.

XX Example 5; Page 213; 215pp; English.

XX The present invention provides the protein and coding sequences of human
CC leukocyte immunoglobulin receptor-like molecules. These can be used as
CC nutritional sources or supplements, or for treating myeloid or lymphoid
CC disorders, burns, wounds, ulcers, Alzheimer's disease, amyotrophic
CC lateral sclerosis, lung or liver fibrosis, immune disorders such as
CC severe combined immunodeficiency, multiple sclerosis, allergies, graft-
CC versus-host disease, inflammations, infertility, stroke, or cancers. The
CC present sequence is a polypeptide described in the exemplification of the
CC invention

XX Sequence 203 AA;

Query Match 74.4%; Score 970; DB 5; Length 203;
Best Local Similarity 100.0%; Pred. No. 4.6e-76;
Matches 183; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRSSRYQDQAVLFIPAMKR 60
DB 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRSSRYQDQAVLFIPAMKR 80
QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120
DB 81 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 140
QY 121 DQFALYKEGDPAPYKKNPERWYRASFPITVTTAAHSGTYRCYFSRSSRDPYLSAPSDPLEL 180
DB 141 DQFALYKEGDPAPYKKNPERWYRASFPITVTTAAHSGTYRCYFSRSSRDPYLSAPSDPLEL 200
QY 181 VVT 183
DB 201 VVT 203

RESULT 4
AAO19236
ID AAO19236 standard; protein; 236 AA.

XX AAO19236;
XX
DT 27-NOV-2002 (first entry)
XX
DE Human LIR-pbm36-2 protein SEQ ID NO: 32.
XX
KW Human; leukocyte immunoglobulin receptor-like protein; LIR-like protein;
KW vulnary; neuroprotective; anti-inflammatory; cerebroprotective;
KW nutritional supplement; lymphoid disorder; burn; wound; ulcer; stroke;
KW Alzheimer's disease; amyotrophic lateral sclerosis; fibrosis; cancer;
KW immune disorder; multiple sclerosis; allergy; inflammation; infertility;
KW cytostatic; immunosuppressive; anti-diabetic; antiinfertility.
XX
OS Homo sapiens.
XX
PN WO200266600-A2.
XX
PD 29-AUG-2002.
XX
PF 28-DEC-2001; 2001WO-US049435.
XX

XX 29-DEC-2000; 2000US-00751518.
PR (HYSE-) HYSEQ INC.
XX Boyle BJ, Kuo C, Mize NK, Haley-Vicente DA, Arterburn MC;
PI Tang YT, Zhou P, Liu C, Asundi V, Drmanac RT, Yeung G, Palencia S;
XX WPI; 2002-674924/72.
XX New leukocyte immunoglobulin receptor-like (LIR-like) polynucleotides and
PT polypeptides, useful in research, as nutritional sources, or for treating
PT wounds, Alzheimer's disease, inflammations, infertility, stroke or
PT cancers.
XX Example 5; Page 190-191; 215pp; English.
PS The present invention provides the protein and coding sequences of human
XX leukocyte immunoglobulin receptor-like molecules. These can be used as
CC nutritional sources or supplements, or for treating myeloid or lymphoid
CC disorders, burns, wounds, ulcers, Alzheimer's disease, amyotrophic
CC lateral sclerosis, lung or liver fibrosis, immune disorders such as
CC severe combined immunodeficiency, multiple sclerosis, allergies, graft-
CC versus-host disease, inflammations, infertility, stroke, or cancers. The
CC present sequence is a polypeptide described in the exemplification of the
CC invention
XX Sequence 236 AA;
SQ Query Match 29.0%; Score 378.5; DB 5; Length 236;
Best Local Similarity 41.7%; Pred. No. 1.5e-24;
Matches 91; Conservative 33; Mismatches 73; Indels 21; Gaps 7;
Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRL--EKLSS---SRYQDQAV--- 52
Db 22 QAGTLPKPTLWAEPGSVITQGSPVTLWCQGILETQYRRLYREKKTAPWITRIPOEIVKKG 81
Qy 53 -LFIPAMKRSLAGRYCSYQNGSL-WSLPDQLELVATGVFAKPSLSAQPGPAVSSGGDV 110
Db 82 QFPIPSITWEHTGRYCRFYGSHTAGWSEPSDPLELVVTGAYIKPTLSALPSPVVTSGNV 141
Qy 111 TLQCQTRYGFDQFALYKEGD---PAPYKNPER---WYRASFPITVTAHSGTYRCYSFS 164
Db 142 TLHCVSQVAFGSFILCKEGEDEHPQLNSQPRTHGWSRAIFSVGPVSPRRWSYRCYAYD 201
Qy 165 SRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAE 202
Db 202 SNSPHVWSLPDLELLVPGAETLS-----PPQNKSD 234
RESULT 5
AAE19107
ID AAE19107 standard; protein; 237 AA.
XX
AC AAE19107;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human NKp46 (isoform b) protein.
XX
KW Human; natural killer cell activating protein; NKp46; therapy; virucide;
KW viral infection; natural killer cell; NK; NKp44; imaging agent; cancer;
KW detection; carcinoma; melanoma; lymphoma; sarcoma; cytostatic.
XX Homo sapiens.
OS
XX WO200208287-A2.
XX
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-IL000664.
XX
XX 20-JUL-2000; 2000IL-00137419.
PR

XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
PA (UYNE) UNIV BEN-GURION NEGEV.
XX
PI Mandelboim O, Porgador A;
XX WPI; 2002-195870/25.
DR N-PSDB; AAD30464.
XX
PT New targeting complex capable of targeting an active substance to a
PT target cell, comprising a target recognition segment and an active
PT segment, useful for treating pathologies associated with viral infections
PT or cancer.
XX
PS Claim 3; Page 104-105; 113pp; English.
XX
CC The invention relates to compositions and methods for the treatment and
CC detection of a variety of viral infections, by using complex agents
CC comprising the natural killer (NK) cells activating proteins, NKp46 and
CC NKp44 and functional fragments thereof, linked to therapeutic or imaging
CC agents. The complex is useful for treating pathologies associated with
CC viral infections (e.g. infections caused by influenza virus, HIV, Epstein
CC -Barr virus, cytomegalovirus, vaccinia virus, ECMV, MVM or herpes virus)
CC and cancer (e.g. carcinomas, melanomas, lymphomas and sarcomas), and for
CC the imaging and monitoring of cancer. The complex may also be used to
CC detect the presence of abnormal cells in a sample. The antibodies can be
CC used to qualitatively or quantitatively detect the ligand for the
CC complex. The present sequence is human NKp46 (isoform b) protein
XX
SQ Sequence 237 AA;
Query Match 27.3%; Score 355.5; DB 5; Length 237;
Best Local Similarity 38.4%; Pred. No. 1.5e-22;
Matches 81; Conservative 30; Mismatches 77; Indels 23; Gaps 3;
Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRL-----EKLSSS 45
Db 22 QQOTLEKPFIIWAEPHFVPEKQVTCQGNYGAVYQLHFEGLFAVDRPKPPERINKV 81
Qy 46 RYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSLPDQLELVATGVFAKPSLSAQPGPAVS 105
Db 82 KF-----YIPDMNSRMAGQYSCIYRVGELMSEPSNLLDLVVTETMTPTLSVHPGPEVI 135
Qy 106 SGGDVTLCQCTRYGFDQFALYKEGDPAKYKNPERWYRASFPITVTAHSGTYRCYSFS 165
Db 136 SGKEKVTFCRLDTATSMFLLLKKEGRSSHVQRYGKYGKQAEFFPLGPVTTAHRGTYRC--FGS 193
Qy 166 RDPYLWSAPSDPLELVVTGTSVTPSRLPTEP 196
Db 194 YNNHAWSPFPSEPVKLLVTDIENTSLAPEDP 224
RESULT 6
ADO24405
ID ADO24405 standard; protein; 227 AA.
XX
AC ADO24405;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human PRO87333 protein SEQ ID NO:44.
XX
KW human; PRO; antianaemic; antiarthritic; antiinflammatory; antipsoriatic;
KW antirheumatic; dermatological; immunostimulant; immunosuppressive;
KW osteopathic; vasotropic; immune related disease;
KW inflammatory immune response; rheumatoid arthritis; osteoarthritis;
KW juvenile chronic arthritis; systemic lupus erythematosus;
KW spondyloarthropathy; systemic sclerosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome;
KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune disease; immune-mediated skin disease; bullous skin disease;
KW erythema multiforme; contact dermatitis; psoriasis; lymphadenopathy;
KW splenomegaly; leukopaenia.

XX Homo sapiens.
OS WO2004043397-A2.
XX 27-MAY-2004.
XX 12-NOV-2003; 2003WO-US036002.
XX 12-NOV-2002; 2002US-0425931P.
PR (GETH) GENENTECH INC.
XX Abbas A, Bodary S, Clark H, Wu TD, Schoenfeld J, Wood WI;
PI WPI; 2004-420080/39.
XX N-PSDB; ADO24404.
DR New isolated PRO polypeptide e.g. PRO37544, PRO69493, PRO87327 etc,
XX capable of stimulating an immune response, useful for treating diseases
PT such as rheumatoid arthritis, psoriasis, and leukopenia.
XX Claim 9; SEQ ID NO 44; 326pp; English.
PS The present invention describes an isolated human PRO polypeptide (I).
XX Also described: (1) an isolated PRO nucleic (II) acid encoding (I); (2) a
CC vector (III) comprising (II); (3) a host cell (IV) comprising (III); (4)
CC producing (I); (5) a chimeric molecule (V) comprising (I) fused to a
CC heterologous amino acid sequence; (6) an antibody (VI) which specifically
CC binds to (I); (7) a composition of matter comprising (I), an agonist of
CC (I), an antagonist of (I), or (VI) in combination with a carrier; (8)
CC treating (M1) an immune related disorder in a mammal, by administering
CC (I), an agonist of (I), an antagonist of (I), or the antibody (VI); (9)
CC diagnosing an immune related disease in a mammal, by detecting the level
CC of expression of a gene encoding (I) in a test sample of tissue cells
CC obtained from the mammal and in a control sample of known normal tissue
CC cells of the same cell type; (10) identifying a compound that inhibits
CC the activity of (I); (11) identifying a compound (M2) that inhibits the
CC expression of a gene encoding (I); (12) identifying a compound that
CC mimics the activity of (I); and (12) stimulating the immune response in a
CC mammal, by administering (I) or its antagonist to the mammal. (I) has
CC antianaemic, antiarthritic, antiinflammatory, antipsoriatic,
CC antirheumatic, dermatological, immunostimulant, immunosuppressive,
CC osteopathic and vasotropic activities. (I) and (VI) are useful for
CC diagnosing an immune related disease in a mammal. (II) is useful for
CC diagnosing an inflammatory immune response in a mammal. (VI) is useful
CC for determining the presence of (I) in a sample suspected of containing
CC the polypeptide. (M1) is useful for treating mammal having an immune
CC related disorder chosen from rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, systemic lupus erythematosus,
CC spondyloarthropathies, systemic sclerosis, idiopathic inflammatory
CC myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
CC autoimmune haemolytic anaemia, autoimmune or immune-mediated skin
CC diseases including bullous skin diseases, erythema multiforme and contact
CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. The
CC present sequence represents a human PRO protein from the present
XX invention.
SQ Sequence 227 AA;
Query Match 23.0%; Score 300; DB 8; Length 227;
Best Local Similarity 36.6%; Pred. No. 9.4e-18;
Matches 71; Conservative 34; Mismatches 77; Indels 12; Gaps 2;
QY 3 GPLPKPSLQALPSSLVPLEKPVTLRCQPGVDLYRLEKLSRRYQD-----QA 51
Db 12 GDFMPFISAKSSPVIPLDGSVKTCQQAIREAYLTQLMIKNSYREIGRRLLKFWNETDP 71
QY 52 VLFIPAMKRSLAGRYRCSYQNSLWSLPSDQLVATGVFAKPSLSAQPGPAVSSGGDVT 111
Db 72 EFVIDHMDANKAGRYQCQYRIGHYFRFRYSDTLELVVTGLYKPKFSLADRGLVLMFGENIS 131
QY 112 LQCOTRY-GFDQFALYKEGDPAPYKNPERWYRASPFIIITVTAHSGTYRCYSFSSRDPYL 170

Db 132 LTCSSAHIPFDRFSLAKEGELSLPQHSGEHPANFSLGPDVLNVSGIYRCYGWYNRSPYL 191
QY 171 WSAPSDPELELVVTG 184
Db 192 WSFPPSNALELVVTG 205
RESULT 7
ID ABG10157 standard; protein; 170 AA.
XX AC ABG10157;
XX DT 13-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #10148.
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US008631.
XX PR 31-MAR-2000; 2000US-00540217.
XX PR 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS74344.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX Claim 20; SEQ ID NO 40516; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
XX amino acid sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 170 AA;
Query Match 21.4%; Score 279.5; DB 4; Length 170;
Best Local Similarity 37.7%; Pred. No. 3.9e-16;
Matches 72; Conservative 22; Mismatches 56; Indels 41; Gaps 7;

Qy 7 KPSLQALPSSLVPLEKPVTLRCQGPVGLYRLEKLSRRYQDQAVLFIPAMKRSLAGRY 66
Db 7 KPSFLALPCHLVKSEETVILQCWSVMFEHLLHR-----EGTY 45
Qy 67 RC-----SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYG 119
Db 46 RCYGSVPHSPYQ-----LSAPSDPLDMVTIGLYEKPSLSAQPGPTVQAGENVTLSCSRSS 101
Qy 120 FDQFALYKEGDPAPYKNP-----ERWYRASFPPIITVTAHSGTYRCYSFSSRD-PYLWSA 173
Db 102 YDMYHLSREGEAHERRLPAVRSINGTFQADFPL--GPATHGGTYRCFCG-SFRDAPYEWSN 158
Qy 174 PSDPLELVVTG 184
Db 159 SSDPLLVSVTG 169
RESULT 8
ID AAO19235 standard; protein; 205 AA.
XX AAO19235;
AC AAO19235;
XX 27-NOV-2002 (first entry)
DT Human immunoglobulin-like protein IGSF1 SEQ ID NO: 31.
XX Human immunoglobulin-like protein; LIR-like protein;
KW Human; leukocyte immunoglobulin receptor-like protein; LIR-like protein;
KW vulnerable; neuroprotective; anti-inflammatory; cerebroprotective;
KW nutritional supplement; lymphoid disorder; burn; wound; ulcer; stroke;
KW Alzheimer's disease; amyotrophic lateral sclerosis; fibrosis; cancer;
KW immune disorder; multiple sclerosis; allergy; inflammation; infertility;
KW cytostatic; immunosuppressive; anti-diabetic; antiinfertility.
XX Homo sapiens.
OS Homo sapiens.
XX WO200266600-A2.
PN 29-AUG-2002.
XX 28-DEC-2001; 2001WO-US049435.
PF 29-DEC-2000; 2000US-00751518.
XX (HYSE-) HYSEQ INC.
XX Boyle BJ, Kuo C, Mize NK, Haley-Vicente DA, Arterburn MC;
PI Tang YT, Zhou P, Liu C, Asundi V, Drmanac RT, Yeung G, Palencia S;
XX WPI; 2002-674924/72.
DR New leukocyte immunoglobulin receptor-like (LIR-like) polynucleotides and
XX polypeptides, useful in research, as nutritional sources, or for treating
PT wounds, Alzheimer's disease, inflammations, infertility, stroke or
PT cancers.
XX Example 5; Page 189-190; 215pp; English.
PS The present invention provides the protein and coding sequences of human
XX leukocyte immunoglobulin receptor-like molecules. These can be used as
CC nutritional sources or supplements, or for treating myeloid or lymphoid
CC disorders, burns, wounds, ulcers, Alzheimer's disease, amyotrophic
CC lateral sclerosis, lung or liver fibrosis, immune disorders such as
CC severe combined immunodeficiency, multiple sclerosis, allergies, graft-
CC versus-host disease, inflammations, infertility, stroke, or cancers. The
CC present sequence is a polypeptide described in the exemplification of the
CC invention
XX Sequence 205 AA;
SQ Query Match 21.1%; Score 275.5; DB 5; Length 205;
Best Local Similarity 38.1%; Pred. No. 1.1e-15;

Matches 75; Conservative 25; Mismatches 84; Indels 13; Gaps 5;
Qy 6 PKPSLQALPSSLVPLEKPVTLRCQGP---PGVDLYRLEKLSRRY-----QDQAVLFIPAM 58
Db 1 PKPWLFAEPSSVVPMGQNVTLWCRGPVHGVGYILHKEGEATSMQLWGSTSDGAFPITNI 60
Qy 59 KRSLAGRYRCYQ---NGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQ 115
Db 61 SGTSMGRYSCCYHPDWTSSIKIQPSNTLELLVTGLLPKPSLLAQPGPMVAPGENMTLQCQ 120
Qy 116 TRYGFQFALYKEG--DPAPYKNPERWYRASFPPIITVTAHSGTYRCYSFSSRDPYLWSA 173
Db 121 GELPDSTFVLLKEGAQEPLEQQRPS-GYRADFWMPAVRGEDSGIYSCVYILDSTPPFAASN 179
Qy 174 PSDPLELVVTGTSVTPS 190
Db 180 HSDSLEIWWTDKPKKPS 196
RESULT 9
ID AAY72789 standard; protein; 74 AA.
XX AAY72789;
AC AAY72789;
XX 31-MAY-2001 (first entry)
DT Human platelet membrane glycoprotein VI (GPVI) partial protein #b.
XX Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
KW vascular disease; thrombosis.
XX Homo sapiens.
OS Homo sapiens.
XX Key Location/Qualifiers
FT Misc-difference 15 /note= "Encoded by CYG"
FT WO200116321-A1.
XX 08-MAR-2001.
PN 01-SEP-2000; 2000WO-US023975.
XX 01-SEP-1999; 99US-0152197P.
PR 08-OCT-1999; 99US-0158251P.
XX (SAKA) OTSUKA PHARM CO LTD.
XX Tandon N, Sun B, Nakamura T, Yamamoto N;
PI WPI; 2001-226691/23.
XX N-PSDB; AAD02854.
DR Anti-thrombotic medicament, comprising a polypeptide having the
XX extracellular domain of platelet membrane glycoprotein VI or its variant,
PT useful for treating a vascular disease and reducing platelet activation.
PT Disclosure; Fig 2; 74pp; English.
PS The present sequence is a human platelet membrane glycoprotein VI (GPVI)
XX partial protein #b. The medicament comprising GPVI is useful for treating
CC vascular disease, and for reducing platelet activation which involves
CC contacting platelets with the medicament. The extracellular portion of
CC GPVI is used therapeutically to attenuate platelet activation and
CC aggregation and to treat thrombosis and other vascular diseases.
CC Antibodies generated against GPVI are used as research and
CC immunotherapeutic agents
XX Sequence 74 AA;
SQ Query Match 20.9%; Score 272; DB 4; Length 74;
Best Local Similarity 98.1%; Pred. No. 5.9e-16;

Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDQAVLF 54
 Db 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYHDAQVLF 74

RESULT 10
 AAY72788
 ID AAY72788 standard; protein; 74 AA.
 XX AC
 XX AAY72788;
 DT 31-MAY-2001 (first entry)
 XX Human platelet membrane glycoprotein VI (GPVI) partial protein #a.
 XX Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
 KW vascular disease; thrombosis.
 XX Homo sapiens.
 OS
 XX
 XX Location/Qualifiers
 FT Misc-difference 15
 FT /note= "Encoded by CYG"
 XX
 PN WO200116321-A1.
 XX
 PD 08-MAR-2001.
 XX
 PF 01-SEP-2000; 2000WO-US023975.
 XX
 PR 01-SEP-1999; 99US-0152197P.
 PR 08-OCT-1999; 99US-0158251P.
 XX
 PA (SAKA) OTSUKA PHARM CO LTD.
 XX
 XX Tandon N, Sun B, Nakamura T, Yamamoto N;
 PI
 XX WPI; 2001-226691/23.
 DR N-PSDB; AAD02854.
 XX
 PT Anti-thrombotic medicament, comprising a polypeptide having the
 PT extracellular domain of platelet membrane glycoprotein VI or its variant,
 PT useful for treating a vascular disease and reducing platelet activation.
 XX
 PS Claim 11; Fig 2; 74pp; English.
 XX
 CC The present sequence is a human platelet membrane glycoprotein VI (GPVI)
 CC partial protein #a. The medicament comprising GPVI is useful for treating
 CC vascular disease, and for reducing platelet activation which involves
 CC contacting platelets with the medicament. The extracellular portion of
 CC GPVI is used therapeutically to attenuate platelet activation and
 CC aggregation and to treat thrombosis and other vascular diseases.
 CC Antibodies generated against GPVI are used as research and
 CC immunotherapeutic agents
 XX
 SQ Sequence 74 AA;

Query Match 20.9%; Score 272; DB 4; Length 74;
 Best Local Similarity 98.1%; Pred. No. 5.9e-16;
 Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYQDQAVLF 54
 Db 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSRRYHDAQVLF 74

RESULT 11
 AAB61259
 ID AAB61259 standard; protein; 47 AA.
 XX AC
 XX AAB61259;

DE Human TANGO 268 IgG like domain #2.

XX Human; mouse; variable heavy; VH; antigen; cancer;

KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;

KW TANGO 268; extracellular matrix; collagen; platelet release;

KW proliferation; migration; embryogenesis; inflammation; thrombosis;

KW degranulation; thrombocytopaenia; antibody; thrombotic disorder;

KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;

KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;

KW cardiovascular disease; angina pectoris; myocardial infarction;

KW coronary restenosis; atherosclerosis; immunological disorder;

KW developmental disorder; embryonic disorder; liver disease;

KW cerebral vascular disease; venous thromboembolism disease.

XX Homo sapiens.

OS WO200280968-A1.

XX 17-OCT-2002.

XX 09-APR-2002; 2002WO-US011122.

XX 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchencker W;

PI Gill DS, Qian DM, Kingsbury G;

PI WPI; 2003-058477/05.

DR Novel substantially purified antibody immunospecifically binding to TANGO

XX 268 antigen, useful for treating bleeding disorders such as

PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

XX Disclosure; Page 212; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable

CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;

CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically

CC binding to a TANGO 268 (also referred as glycoprotein VI (GpVI)) antigen.

CC The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet

CC release and aggregating blocker. The antibodies of the invention are

CC useful for modulating proliferation, migration, morphology,

CC differentiation and/or function of megakaryocytes and platelets,

CC including during development e.g. embryogenesis, modulating leukocyte-

CC platelet and platelet-endothelium interactions in inflammation and/or

CC thrombosis, and modulating platelet aggregation and degranulation. They

CC are also useful for modulating disorders associated with abnormal or

CC aberrant megakaryocyte and/or platelet proliferation, migration,

CC morphology, differentiation and/or function, e.g. bleeding disorders such

CC as thrombocytopaenia. Other diseases which may be modulated by these

CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.

CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases

CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);

CC coronary diseases (e.g. cardiovascular diseases including angina

CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,

CC etc); immunological disorders, developmental disorders, embryonic

CC disorders, liver disorders, cerebral vascular diseases, venous

CC thromboembolism disease, coronary diseases, and metastatic cancers. The

CC antibodies of the invention only causes a transient decrease in platelet

CC counts, platelet aggregation, and/or platelet activation and so have some

CC advantages over prior art methods. The present sequence represents a

CC peptide sequence used to generate the antibodies of the invention

XX Sequence 47 AA;

SQ Query Match 20.6%; Score 268; DB 6; Length 47;

Best Local Similarity 100.0%; Pred. No. 7.3e-16;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 160

Db 1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47

RESULT 13

AAO19267

ID AAO19267 standard; protein; 228 AA.

XX AAO19267;

AC AAO19267;

XX 27-NOV-2002 (first entry)

XX Human FcR-II protein SEQ ID NO: 76.

XX Human; leukocyte immunoglobulin receptor-like protein; LIR-like protein;

KW vulnery; neuroprotective; anti-inflammatory; cerebroprotective;

KW nutritional supplement; lymphoid disorder; burn; wound; ulcer; stroke;

KW Alzheimer's disease; amyotrophic lateral sclerosis; fibrosis; cancer;

KW immune disorder; multiple sclerosis; allergy; inflammation; infertility;

KW cytostatic; immunosuppressive; anti-diabetic; antiinfertility.

XX Homo sapiens.

OS WO200266600-A2.

XX 29-AUG-2002.

XX 28-DEC-2001; 2001WO-US049435.

XX 29-DEC-2000; 2000US-00751518.

XX (HYSE-) HYSEQ INC.

XX Boyle BJ, Kuo C, Mize NK, Haley-Vicente DA, Arterburn MC;

PI Tang YT, Zhou P, Liu C, Asundi V, Drmanac RT, Yeung G, Palencia S;

XX WPI; 2002-674924/72.

XX New leukocyte immunoglobulin receptor-like (LIR-like) polynucleotides and

PT polypeptides, useful in research, as nutritional sources, or for treating

PT wounds, Alzheimer's disease, inflammations, infertility, stroke or

PT cancers.

XX Example 5; Page 213-214; 215pp; English.

XX The present invention provides the protein and coding sequences of human

CC leukocyte immunoglobulin receptor-like molecules. These can be used as

CC nutritional sources or supplements, or for treating myeloid or lymphoid

CC disorders, burns, wounds, ulcers, Alzheimer's disease, amyotrophic

CC lateral sclerosis, lung or liver fibrosis, immune disorders such as

CC severe combined immunodeficiency, multiple sclerosis, allergies, graft-

CC versus-host disease, inflammations, infertility, stroke, or cancers. The

CC present sequence is a polypeptide described in the exemplification of the

CC invention

XX Sequence 228 AA;

SQ Query Match 18.8%; Score 245; DB 5; Length 228;

Best Local Similarity 34.8%; Pred. No. 5.7e-13;

Matches 65; Conservative 30; Mismatches 74; Indels 18; Gaps 6;

QY 6 PKPSLQALPSSLVPLEKPVTLRCQPPGV---DLYKLEKLSRRYQD---QAVLFIPAM 58

Db 1 PKPWLGAQPATVVTGPNVTLRCRAPQPAWRFGLFKPGEIAPLLFRDVSSELAEFFLEEV 60

QY 59 KRSLAGRYRCSYQ-----NGSLWSLPSDQLELVATGVFAKPSLSAQPGFVSSGGDVTLQC 114

Db 61 TPAQGGSYRCCYRRRPNWGPVWSQPSDVLELLVTEELPRPSLVALPGFVVGPGANVSLRC 120

QY 115 QTRYGFDQFALYKEGDPAPYK---NPERWYRASFPFIITVTAHSGTYRCYFSRRDPYLW 171

Db 121 AGLRNMSFVLYREGVAAPLOYRHSAPW--ADFTLLGARA--PGTYSCTYHTPSAPYVL 176

QY 172 SAPSDPL 178
Db 177 SQRSEVL 183

RESULT 14
AAO19233
ID AAO19233 standard; protein; 145 AA.
XX
AC AAO19233;
XX
DT 27-NOV-2002 (first entry)
XX
DE Human putative inhibitory receptor SEQ ID NO: 29.
XX
KW Human; leukocyte immunoglobulin receptor-like protein; LIR-like protein;
KW vulnerable; neuroprotective; anti-inflammatory; cerebroprotective;
KW nutritional supplement; lymphoid disorder; burn; wound; ulcer; stroke;
KW Alzheimer's disease; amyotrophic lateral sclerosis; fibrosis; cancer;
KW immune disorder; multiple sclerosis; allergy; inflammation; infertility;
KW cytostatic; immunosuppressive; anti-diabetic; antiinfertility.
XX
OS Homo sapiens.
XX
PN WO200266600-A2.
XX
PD 29-AUG-2002.
XX
PF 28-DEC-2001; 2001WO-US049435.
XX
PR 29-DEC-2000; 2000US-00751518.
XX
PA (HYSE-) HYSEQ INC.
PI Boyle BJ, Kuo C, Mize NK, Haley-Vicente DA, Arterburn MC;
PI Tang YT, Zhou P, Liu C, Asundi V, Drmanac RT, Yeung G, Palencia S;
XX
DR WPI; 2002-674924/72.
XX
XX New leukocyte immunoglobulin receptor-like (LIR-like) polynucleotides and
PT polypeptides, useful in research, as nutritional sources, or for treating
PT wounds, Alzheimer's disease, inflammations, infertility, stroke or
PT cancers.
XX
PS Example 5; Page 188-189; 215pp; English.
XX
CC The present invention provides the protein and coding sequences of human
CC leukocyte immunoglobulin receptor-like molecules. These can be used as
CC nutritional sources or supplements, or for treating myeloid or lymphoid
CC disorders, burns, wounds, ulcers, Alzheimer's disease, amyotrophic
CC lateral sclerosis, lung or liver fibrosis, immune disorders such as
CC severe combined immunodeficiency, multiple sclerosis, allergies, graft-
CC versus-host disease, inflammations, infertility, stroke, or cancers. The
CC present sequence is a polypeptide described in the exemplification of the
CC invention.

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGD---LYRLEKLS--SRVQD---QAV 52
Db 22 QAGHLPKPTLWAEPSGVIIQGPSVTLRCQGSLOAEYHLYRENKSASWVRRIQEPGKNGQ 81

QY 53 LFTIPAMKRSAGRYRCSYONGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTL 112
Db 82 FPIPSITWEHAGRYHCQYSHNSSEYSDPLELVVTGAYSKPTLSALPSPVVTGGNVTL 141

QY 113 QC 114
Db 142 QC 143

Query Match 17.9%; Score 233; DB 5; Length 145;
Best Local Similarity 46.7%; Pred. No. 3.5e-12;
Matches 57; Conservative 16; Mismatches 41; Indels 8; Gaps 3;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGD---LYRLEKLS--SRVQD---QAV 52
Db 22 QAGHLPKPTLWAEPSGVIIQGPSVTLRCQGSLOAEYHLYRENKSASWVRRIQEPGKNGQ 81

QY 53 LFTIPAMKRSAGRYRCSYONGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTL 112
Db 82 FPIPSITWEHAGRYHCQYSHNSSEYSDPLELVVTGAYSKPTLSALPSPVVTGGNVTL 141

QY 113 QC 114
Db 142 QC 143

Query Match 17.9%; Score 233; DB 5; Length 145;
Best Local Similarity 46.7%; Pred. No. 3.5e-12;
Matches 57; Conservative 16; Mismatches 41; Indels 8; Gaps 3;

RESULT 15
ABB42669
ID ABB42669 standard; peptide; 100 AA.
XX
AC ABB42669;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #10175 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000669.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
PS Claim 27; SEQ ID NO 35304; 639pp + Sequence Listing; English.
XX
CC The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

QY 91 FAKPSLSAQPGPAVSSGGDVTLCQTRYGDFQFALYKEG---DP----APYKNPERWYRA 143
Db 3 YDRVSLSVQPGPTVASEGVNTLLCQSQGMWMTFLLTKEGAADDPWRLRSTYQSK--YQA 60

QY 144 SFPIITVTAHSGTYRCYCSFSSRDPYLWSAPSDPLELVVT 183
Db 61 EFPMPVTSAHAGTYRCYCSQSSKPYLLTHPSDPLELVVS 100

RESULT 16
AAM36482
ID AAM36482 standard; protein; 100 AA.
XX
AC AAM36482;
XX
DT 17-OCT-2001 (first entry)
XX

Query Match 17.4%; Score 227.5; DB 4; Length 100;
Best Local Similarity 50.0%; Pred. No. 6.5e-12;
Matches 50; Conservative 16; Mismatches 25; Indels 9; Gaps 3;

QY 91 FAKPSLSAQPGPAVSSGGDVTLCQTRYGDFQFALYKEG---DP----APYKNPERWYRA 143
Db 3 YDRVSLSVQPGPTVASEGVNTLLCQSQGMWMTFLLTKEGAADDPWRLRSTYQSK--YQA 60

QY 144 SFPIITVTAHSGTYRCYCSFSSRDPYLWSAPSDPLELVVT 183
Db 61 EFPMPVTSAHAGTYRCYCSQSSKPYLLTHPSDPLELVVS 100

RESULT 16
AAM36482
ID AAM36482 standard; protein; 100 AA.
XX
AC AAM36482;
XX
DT 17-OCT-2001 (first entry)
XX

Query Match 17.4%; Score 227.5; DB 4; Length 100;
Best Local Similarity 50.0%; Pred. No. 6.5e-12;
Matches 50; Conservative 16; Mismatches 25; Indels 9; Gaps 3;

DE Peptide #10519 encoded by probe for measuring placental gene expression.
XX
KW Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 36751; 654pp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AAI31315-AAI57546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 100 AA;

Query Match 17.4%; Score 227.5; DB 4; Length 100;
Best Local Similarity 50.0%; Pred. No. 6.5e-12;
Matches 50; Conservative 16; Mismatches 25; Indels 9; Gaps 3;

QY 91 FAKPSLSAQPGPAVSSGGDVTLCQCTRYGFDQFALYKEG---DP-----APYKNPERWYRA 143
Db : : ||| ||||| :|| :||| ||:: || ||| || ||| :|| : : ||:
3 YDRVSLSVQPGPTVASGENVTLLCQSQGMMQTFLLTKEGAADDPWRLRSTYQSQK--YQA 60

QY 144 SFPIITVTAHSGTYRCYSFSSRDPYLWSAPSDPLELVVT 183
Db ||: ||: ||: ||||| | ||| : ||||| |||:
61 EFPMPGVTSAHAGTYRCYGSQSSKPYLLTHPSDPLELVVS 100

RESULT 17
ABB26006
ID ABB26006 standard; protein; 100 AA.
XX
AC ABB26006;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #8005 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.
PF
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
PT hearts.
XX
PS Claim 15; SEQ ID NO 27776; 530pp; English.
XX
CC The present invention relates to single exon nucleic acid probes for
CC measuring human gene expression in a sample derived from human heart (see
CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
CC probe. The probes may be used for predicting, measuring and displaying
CC gene expression in samples derived from the human heart via microarrays.
CC By measuring gene expression, the probes are useful for predicting, the
CC diagnosing, grading, staging, monitoring and prognosing diseases of the
CC human heart and vascular system e.g. cardiovascular disease,
CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 100 AA;

Query Match 17.4%; Score 227.5; DB 4; Length 100;
Best Local Similarity 50.0%; Pred. No. 6.5e-12;
Matches 50; Conservative 16; Mismatches 25; Indels 9; Gaps 3;

QY 91 FAKPSLSAQPGPAVSSGGDVTLCQCTRYGFDQFALYKEG---DP-----APYKNPERWYRA 143
Db : : ||| ||||| :|| :||| ||:: || ||| || ||| :|| : : ||:
3 YDRVSLSVQPGPTVASGENVTLLCQSQGMMQTFLLTKEGAADDPWRLRSTYQSQK--YQA 60

QY 144 SFPIITVTAHSGTYRCYSFSSRDPYLWSAPSDPLELVVT 183
Db ||: ||: ||: ||||| | ||| : ||||| |||:
61 EFPMPGVTSAHAGTYRCYGSQSSKPYLLTHPSDPLELVVS 100

RESULT 18
AAM76374
ID AAM76374 standard; protein; 100 AA.
XX
AC AAM76374;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 36680.
XX
KW Human; bone marrow expressed exon; gene expression analysis; probe;
KW microarray; cancer; leukaemia; lymphoma; myeloma.
XX
OS Homo sapiens.
XX
PN WO200157276-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000668.
XX
PN 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.

CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (I) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 100 AA;

Query Match 17.4%; Score 227.5; DB 4; Length 100;
Best Local Similarity 50.0%; Pred. No. 6.5e-12;
Matches 50; Conservative 16; Mismatches 25; Indels 9; Gaps 3;

Qy 91 FAKPSLSAQPGPAVSSGGDVTLCQCTRYGFDQFALYKEG---DP-----APYKNPERWYRA 143
Db 3 YDRVSLSVQPGPTVASGENVTLLCQSQGWMQTFLLTKEGAADPWRLRSTYQSK--YQA 60

Qy 144 SFPIITVTAHSGTYRCYCSFSSRDPYLWSAPSDPLELVVT 183
Db 61 EFPMPVTSAHAGTYRCYCSQSSKPYLLTHPSDPLELVVS 100

RESULT 21
ABG45662
ID ABG45662 standard; peptide; 100 AA.
XX
AC ABG45662;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 35327.
XX
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karagener syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US0000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX WPI; 2002-114183/15.
DR
XX Spatially-addressable set of single exon nucleic acid probes, used to
PT measure gene expression in human lung samples.
XX
PS Claim 27; SEQ ID NO 35327; 634pp; English.
XX

CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human lung comprising single exon nucleic acid probes having one of
CC 12614 nucleic acid sequences mentioned in the specification, or their
CC complements or the 12387 open reading frames derived from the 12614
CC probes. Also included are a microarray comprising the novel set of probes
CC ; the novel set of probes which hybridise at high stringency to a nucleic
CC acid expressed in the human lung; measuring gene expression in a sample
CC derived from human lung, comprising (a) contacting the array with a
CC collection of detectably labeled nucleic acids derived from human lung
CC mRNA, and (b) measuring the label detectably bound to each probe of the
CC array; identifying exons in a eukaryotic genome, comprising (a)
CC algorithmically predicting at least one exon from genomic sequences of
CC the eukaryote; and (b) detecting specific hybridisation of detectably
CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
CC having a fragment identical to the predicted exon, the probe is included
CC in the above mentioned microarray; assigning exons to a single gene,
CC comprising (a) identifying exons from genomic sequence by the method
CC above and (b) measuring the expression of each of the exons in several
CC tissues and/or cell types using hybridisation to a single exon
CC microarrays having a probe with the exon, where a common pattern of
CC expression of the exons in the tissues and/or cell types indicates that
CC the exons should be assigned to a single gene; a peptide comprising one
CC of 12011 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
CC Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a peptide/protein encoded by a single exon probe of
CC the invention. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 100 AA;

Query Match 17.4%; Score 227.5; DB 5; Length 100;
Best Local Similarity 50.0%; Pred. No. 6.5e-12;
Matches 50; Conservative 16; Mismatches 25; Indels 9; Gaps 3;

Qy 91 FAKPSLSAQPGPAVSSGGDVTLCQCTRYGFDQFALYKEG---DP-----APYKNPERWYRA 143
Db 3 YDRVSLSVQPGPTVASGENVTLLCQSQGWMQTFLLTKEGAADPWRLRSTYQSK--YQA 60

Qy 144 SFPIITVTAHSGTYRCYCSFSSRDPYLWSAPSDPLELVVT 183
Db 61 EFPMPVTSAHAGTYRCYCSQSSKPYLLTHPSDPLELVVS 100

RESULT 22
AAB61272
ID AAB61272 standard; protein; 47 AA.
XX
AC AAB61272;
XX
DT 04-APR-2001 (first entry)
XX
DE Mouse TANGO 268 Ig-like domain #2.
XX
KW Mouse; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Mus musculus.
XX

PN WO200100810-A1.
XX
XX PD 04-JAN-2001.
XX PF 30-JUN-2000; 2000WO-US018152.
XX PR 30-JUN-1999; 99US-00345468.
XX PR 06-DEC-1999; 99US-00454824.
XX PR 14-FEB-2000; 2000US-00503387.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchencker W;
PI Gill DS, Qian MD, Kingsbury G;
XX
XX DR WPI; 2001-080877/09.
XX
XX PT New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating and
PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological
PT disorders.
XX
XX PS Disclosure; Page 210-211; 227pp; English.
XX
XX CC The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders (e.g.
CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
CC immunological diseases (e.g. platelet disorder) and embryonic liver
CC disorders. Preferably they are used to prevent acute cardiac ischaemia
CC following angioplasty and metastatic cancers, especially of the colon and
CC liver
XX
XX SQ Sequence 47 AA;

Query Match 16.9%; Score 220; DB 4; Length 47;
Best Local Similarity 78.7%; Pred. No. 1.1e-11;
Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPIITVTAHSGTYRC 160
Db 1 CQSPYSFDEFVLVYKEGDTGPKRPEKWKYRANFPPIITVTAHSGTYRC 47

RESULT 23
ABU11238
ID ABU11238 standard; peptide; 47 AA.
XX
AC ABU11238;
XX
XX 06-FEB-2003 (first entry)
XX
XX TANGO 268 IgG like domain #2.
DE
XX
KW Human; mouse; variable heavy; VH; antigen; cancer;
KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
KW TANGO 268; extracellular matrix; collagen; platelet release;
KW proliferation; migration; embryogenesis; inflammation; thrombosis;
KW degranulation; thrombocytopaenia; antibody; thrombotic disorder;
KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
KW cardiovascular disease; angina pectoris; myocardial infarction;
KW coronary restenosis; atherosclerosis; immunological disorder;
KW developmental disorder; embryonic disorder; liver disorder;
KW cerebral vascular disease; venous thromboembolism disease.

OS Mus musculus.
XX
XX PN WO200280968-A1.
XX PD 17-OCT-2002.
XX PF 09-APR-2002; 2002WO-US011122.
XX PR 09-APR-2001; 2001US-00829495.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX
XX PI Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchencker W;
PI Gill DS, Qian DM, Kingsbury G;
XX
XX DR WPI; 2003-058477/05.
XX
XX PT Novel substantially purified antibody immunospecifically binding to TANGO
PT 268 antigen, useful for treating bleeding disorders such as
PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.
XX
XX PS Disclosure; Page 219; 236pp; English.
XX
XX CC This invention relates to a novel purified antibody comprising a variable
CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
CC The antibodies of the invention act to decrease or block TANGO 268
CC binding to extracellular matrix components, or as a Collagen or platelet
CC release and aggregation blocker. The antibodies of the invention are
CC useful for modulating proliferation, migration, morphology,
CC differentiation and/or function of megakaryocytes and platelets,
CC including during development e.g. embryogenesis, modulating leukocyte-
CC platelet and platelet-endothelium interactions in inflammation and/or
CC thrombosis, and modulating platelet aggregation and degradation. They
CC are also useful for modulating disorders associated with abnormal or
CC aberrant megakaryocyte and/or platelet proliferation, migration,
CC morphology, differentiation and/or function, e.g. bleeding disorders such
CC as thrombocytopaenia. Other diseases which may be modulated by these
CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
CC coronary diseases (e.g. cardiovascular diseases including angina
CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
CC etc); immunological disorders, developmental disorders, embryonic
CC disorders, liver disorders, cerebral vascular diseases, venous
CC thromboembolism disease, coronary diseases, and metastatic cancers. The
CC antibodies of the invention only causes a transient decrease in platelet
CC counts, platelet aggregation, and/or platelet activation and so have some
CC advantages over prior art methods. The present sequence represents a
CC peptide sequence used to generate the antibodies of the invention
XX
XX SQ Sequence 47 AA;

Query Match 16.9%; Score 220; DB 6; Length 47;
Best Local Similarity 78.7%; Pred. No. 1.1e-11;
Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPIITVTAHSGTYRC 160
Db 1 CQSPYSFDEFVLVYKEGDTGPKRPEKWKYRANFPPIITVTAHSGTYRC 47

RESULT 24
ADK98546
ID ADK98546 standard; protein; 221 AA.
XX
AC ADK98546;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human immune response associated protein IRAP-9 protein.
DE
XX

KW immune response associated protein; IRAP; antiarteriosclerotic;
KW cytostatic; neuroprotective; antiparkinsonian; hepatotropic;
KW cerebroprotective; antiinflammatory; nootropic; vasotropic;
KW arteriosclerosis; cirrhosis; cancer; stroke; Alzheimer's disease;
KW Parkinson's; Crohn's; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO2004020593-A2.
XX
PD 11-MAR-2004.
XX
PF 26-AUG-2003; 2003WO-US026988.
XX
XX 30-AUG-2002; 2002US-0407561P.
PR 11-SEP-2002; 2002US-0410178P.
PR 13-SEP-2002; 2002US-0410571P.
PR 18-OCT-2002; 2002US-0419906P.
PR 25-OCT-2002; 2002US-0421445P.
XX
PA (INCY-) INCYTE CORP.
XX
XX Ramkumar J, Swarnakar A, Elliott VS, Hafalia AJA, Richardson TW;
PI Lee SY, Lindquist EA, Marquis JP, Chawla NK, Khare R, Becha SD;
PI
XX
DR WPI; 2004-239178/22.
DR N-PSDB; ADK98581.
XX
XX New isolated immune response associated proteins (IRAP) polypeptide and
PT polynucleotide, useful for diagnosing and/or treating disorders with
PT aberrant expression of IRAP, such as arteriosclerosis, cirrhosis, cancer
PT and stroke.
XX
PS Claim 1; SEQ ID NO 9; 207pp; English.
XX
XX The invention relates to a novel isolated immune response associated
CC protein (IRAP) comprising any of 35 fully defined sequences given in the
CC specification. The polypeptide of the invention demonstrates
CC antiarteriosclerotic, cytostatic, neuroprotective, antiparkinsonian,
CC hepatotropic, cerebroprotective, antiinflammatory, nootropic and
CC vasotropic activities and may be useful for treating a disease or
CC condition associated with decreased expression or overexpression of
CC functional immune response associated proteins, while the antibody is
CC useful for diagnosing a condition or disease associated with the
CC expression of IRAP, such as arteriosclerosis, cirrhosis, cancer, stroke,
CC Alzheimer's disease, Parkinson's disease and Crohn's disease.
CC Furthermore, the molecules of the invention may be utilised during gene
CC therapy procedures. The current sequence is that of a human IRAP protein
CC of the invention.
XX
SQ Sequence 221 AA;

Query Match 16.8%; Score 218.5; DB 8; Length 221;
Best Local Similarity 31.7%; Pred. No. 1.1e-10;
Matches 60; Conservative 32; Mismatches 80; Indels 17; Gaps 3;

Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVLDLYRLEKLSSSRYQD----- 49
Db 22 QEGDFNPFIFISAKSSPVIPLDGSVKIQCAIREAYLTQLMIKNSTYREIGRRLLKFWNET 81
Qy 50 QAVLFIPAMKRSLAGRVCYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGD 109
Db 82 DPEFVIDHMDANKAGRVQCQYRIGHYFRYSDTLELVVTGLYKPFLSADRGLVLMFGEN 141
Qy 110 VTLCQCTRY-GFDQFALYKEGDPAPYKNPERWYRASFIITVTAHSGTYRCYSFSSRDP 168
Db 142 ISLTCSSAHIPDFRFSLAKEGELSLPQHSQGEHPANFSLGPVDLNVSGIYRLH-----PP 196
Qy 169 YLWSAPSDP 177
Db 197 RLHDAELDP 205

RESULT 25
AAM15998
ID AAM15998 standard; protein; 100 AA.
XX
AC AAM15998;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #2432 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
OS Homo sapiens.
XX
PN WO200157278-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000670.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
(MOLE-) MOLECULAR DYNAMICS INC.
PA
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488901/53.
DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human cervical epithelial cells.
XX
PS Claim 27; SEQ ID NO 20824; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
CC (SENPs: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 100 AA;

Query Match 16.6%; Score 216.5; DB 4; Length 100;
Best Local Similarity 50.0%; Pred. No. 5.9e-11;
Matches 49; Conservative 13; Mismatches 31; Indels 5; Gaps 1;

Qy 91 FAKPSLSAQPGPAVSSGGDVTLCQCTRYGFDQFALYKEGDPAP-----YKNPERWYRAS 145
Db 3 YDRPSLSVQPVPTVAPGKNVTLLCQSRGQFHTFLTKEGAGHPPLHLRSEHQAOQQA 62
Qy 146 PIITVTAHSGTYRCYSFSSRDPYLMWSAPSDPLELVVT 183
Db 63 RMGPVTSAHVGTYRCYSSLSNPNYLLSLPSDPLELVVS 100

Search completed: October 29, 2005, 03:43:59
Job time : 175 secs

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OM protein - protein search, using sw model

Run on: October 29, 2005, 03:47:03 ; Search time 164 Seconds
(without alignments)
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Maximum Match 100%
Listing first 100 summaries

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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1304	100.0	249	9	US-09-832-312-9
2	1304	100.0	249	11	US-09-829-495-9
3	1304	100.0	249	16	US-10-850-034-9
4	355.5	27.3	237	15	US-10-333-481-13
5	279.5	21.4	170	18	US-10-450-763-40516
6	272	20.9	74	14	US-10-446-826-2
7	272	20.9	74	14	US-10-446-826-3
8	272	20.9	74	16	US-10-446-826-2
9	272	20.9	74	16	US-10-446-826-3
10	268	20.6	47	9	US-09-832-312-7
11	268	20.6	47	11	US-09-829-495-7
					Sequence 9, Appli
					Sequence 9, Appli
					Sequence 13, Appli
					Sequence 40516, A
					Sequence 2, Appli
					Sequence 3, Appli
					Sequence 2, Appli
					Sequence 3, Appli
					Sequence 7, Appli
					Sequence 7, Appli

12	268	20.6	47	16	US-10-850-034-7	Sequence 7, Appli
13	227.5	17.4	100	9	US-09-864-761-41304	Sequence 41304, A
14	220	16.9	47	9	US-09-832-312-23	Sequence 23, Appl
15	220	16.9	47	11	US-09-829-495-23	Sequence 23, Appl
16	220	16.9	47	16	US-10-850-034-23	Sequence 23, Appl
17	216.5	16.6	100	9	US-09-864-761-35700	Sequence 35700, A
18	216.5	16.6	100	9	US-09-864-761-36185	Sequence 36185, A
19	216	16.6	41	9	US-09-832-312-6	Sequence 6, Appli
20	216	16.6	41	11	US-09-829-495-6	Sequence 6, Appli
21	216	16.6	41	16	US-10-850-034-6	Sequence 6, Appli
22	213.5	16.4	209	17	US-10-684-206-10	Sequence 10, Appl
23	210.5	16.1	99	9	US-09-864-761-44909	Sequence 44909, A
24	207	15.9	100	9	US-09-864-761-45515	Sequence 45515, A
25	202.5	15.5	100	9	US-09-864-761-45373	Sequence 45373, A
26	195.5	15.0	134	15	US-10-333-481-22	Sequence 22, Appl
27	194	14.9	117	15	US-10-333-481-23	Sequence 23, Appl
28	193.5	14.8	97	14	US-10-029-386-32815	Sequence 32815, A
29	193	14.8	100	9	US-09-864-761-44966	Sequence 44966, A
30	191.5	14.7	97	14	US-10-029-386-30813	Sequence 30813, A
31	187	14.3	50	9	US-09-832-312-13	Sequence 13, Appl
32	187	14.3	50	11	US-09-829-495-13	Sequence 13, Appl
33	187	14.3	50	16	US-10-850-034-13	Sequence 13, Appl
34	179.5	13.8	49	18	US-10-450-763-35200	Sequence 35200, A
35	175	13.4	209	9	US-09-870-759-47	Sequence 47, Appl
36	175	13.4	209	10	US-09-751-708A-47	Sequence 47, Appl
37	175	13.4	209	16	US-10-428-817A-43	Sequence 43, Appl
38	170.5	13.1	152	15	US-10-309-290-102	Sequence 102, App
39	170.5	13.1	159	15	US-10-309-290-104	Sequence 104, App
40	166.5	12.8	89	9	US-09-864-761-48160	Sequence 48160, A
41	165.5	12.7	107	18	US-10-450-763-57511	Sequence 57511, A
42	165.5	12.7	142	15	US-10-309-290-106	Sequence 106, App
43	164	12.6	41	9	US-09-832-312-22	Sequence 22, Appl
44	164	12.6	41	11	US-09-829-495-22	Sequence 22, Appl
45	164	12.6	41	16	US-10-850-034-22	Sequence 26, Appl
46	162.5	12.5	120	15	US-10-333-681-26	Sequence 10, Appl
47	162.5	12.5	135	14	US-10-290-631-10	Sequence 108, App
48	162.5	12.5	135	15	US-10-309-290-108	Sequence 10, Appl
49	162.5	12.5	135	16	US-10-777-524-10	Sequence 10, Appl
50	162.5	12.5	135	17	US-10-777-521-10	Sequence 10, Appl
51	158.5	12.2	178	15	US-10-108-260A-3532	Sequence 3532, App
52	154	11.8	115	20	US-11-111-953-327	Sequence 327, App
53	154	11.8	120	20	US-11-111-953-144	Sequence 144, App
54	152	11.7	86	14	US-10-029-386-33223	Sequence 33223, A
55	140.5	10.8	87	9	US-09-864-761-47449	Sequence 47449, A
56	137.5	10.5	87	9	US-09-864-761-40771	Sequence 40771, A
57	137	10.5	236	15	US-10-291-265-390	Sequence 390, App
58	136.5	10.5	87	9	US-09-864-761-41358	Sequence 41358, A
59	136.5	10.5	87	9	US-09-864-761-45638	Sequence 45638, A
60	136.5	10.5	87	9	US-09-864-761-48765	Sequence 48765, A
61	136	10.4	236	15	US-10-291-265-862	Sequence 862, App
62	135	10.4	236	13	US-10-052-586-544	Sequence 544, App
63	135	10.4	236	14	US-10-174-590-544	Sequence 544, App
64	135	10.4	236	14	US-10-176-758-544	Sequence 544, App
65	135	10.4	236	14	US-10-175-737-544	Sequence 544, App
66	135	10.4	236	14	US-10-174-581-544	Sequence 544, App
67	135	10.4	236	14	US-10-176-483-544	Sequence 544, App
68	135	10.4	236	14	US-10-176-749-544	Sequence 544, App
69	135	10.4	236	14	US-10-176-914-544	Sequence 544, App
70	135	10.4	236	14	US-10-176-915-544	Sequence 544, App
71	135	10.4	236	14	US-10-173-706-544	Sequence 544, App
72	135	10.4	236	14	US-10-175-738-544	Sequence 544, App
73	135	10.4	236	14	US-10-175-752-544	Sequence 544, App
74	135	10.4	236	14	US-10-176-482-544	Sequence 544, App
75	135	10.4	236	14	US-10-176-757-544	Sequence 544, App
76	135	10.4	236	14	US-10-176-913-544	Sequence 544, App
77	135	10.4	236	14	US-10-180-552-544	Sequence 544, App
78	135	10.4	236	14	US-10-180-557-544	Sequence 544, App
79	135	10.4	236	14	US-10-173-700-544	Sequence 544, App
80	135	10.4	236	14	US-10-174-572-544	Sequence 544, App
81	135	10.4	236	14	US-10-174-579-544	Sequence 544, App
82	135	10.4	236	14	US-10-174-582-544	Sequence 544, App
83	135	10.4	236	14	US-10-174-588-544	Sequence 544, App
84	135	10.4	236	14	US-10-175-739-544	Sequence 544, App

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85      135      10.4      236      14      US-10-175-740-544      Sequence 544, App
86      135      10.4      236      14      US-10-175-743-544      Sequence 544, App
87      135      10.4      236      14      US-10-176-488-544      Sequence 544, App
88      135      10.4      236      14      US-10-176-492-544      Sequence 544, App
89      135      10.4      236      14      US-10-176-747-544      Sequence 544, App
90      135      10.4      236      14      US-10-176-750-544      Sequence 544, App
91      135      10.4      236      14      US-10-176-985-544      Sequence 544, App
92      135      10.4      236      14      US-10-176-987-544      Sequence 544, App
93      135      10.4      236      14      US-10-176-992-544      Sequence 544, App
94      135      10.4      236      14      US-10-176-993-544      Sequence 544, App
95      135      10.4      236      14      US-10-184-658-544      Sequence 544, App
96      135      10.4      236      14      US-10-176-991-544      Sequence 544, App
97      135      10.4      236      14      US-10-173-695-544      Sequence 544, App
98      135      10.4      236      14      US-10-173-697-544      Sequence 544, App
99      135      10.4      236      14      US-10-173-705-544      Sequence 544, App
100     135      10.4      236      14      US-10-174-576-544      Sequence 544, App
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ALIGNMENTS

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RESULT 1
US-09-832-312-9
; Sequence 9, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-9
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Query Match      100.0%; Score 1304; DB 9; Length 249;
Best Local Similarity 100.0%; Pred. No. 9.7e-96;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1      QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSSSRYQDQAVLFIPAMKR 60
      |||
Db      1      QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSSSRYQDQAVLFIPAMKR 60

Qy      61      SLAGRYRCYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120
      |||
Db      61      SLAGRYRCYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120

Qy      121     DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYFSFSSRDPYLWSAPSDPLEL 180
      |||
Db      121     DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYFSFSSRDPYLWSAPSDPLEL 180

Qy      181     VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSPPKESDSPAGP 240
      |||
Db      181     VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSPPKESDSPAGP 240

Qy      241     ARQYVTKGN 249
      |||
Db      241     ARQYVTKGN 249

RESULT 2
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US-09-829-495-9
; Sequence 9, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villeva J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-9

Query Match      100.0%; Score 1304; DB 11; Length 249;
Best Local Similarity 100.0%; Pred. No. 9.7e-96;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1      QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSSSRYQDQAVLFIPAMKR 60
      |||
Db      1      QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVDLYRLEKLSSSRYQDQAVLFIPAMKR 60

Qy      61      SLAGRYRCYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120
      |||
Db      61      SLAGRYRCYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGF 120

Qy      121     DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYFSFSSRDPYLWSAPSDPLEL 180
      |||
Db      121     DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYFSFSSRDPYLWSAPSDPLEL 180

Qy      181     VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSPPKESDSPAGP 240
      |||
Db      181     VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSPPKESDSPAGP 240

Qy      241     ARQYVTKGN 249
      |||
Db      241     ARQYVTKGN 249

RESULT 3
US-10-850-034-9
; Sequence 9, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villeva J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-850-034-9

Query Match 100.0%; Score 1304; DB 16; Length 249;
Best Local Similarity 100.0%; Pred. No. 9.7e-96;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVDLRLKLSRRYQDQAVLFIPAMKR 60
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVDLRLKLSRRYQDQAVLFIPAMKR 60

QY 61 SLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQPGPAVSSGGVTLQCOTRYGF 120
Db 61 SLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQPGPAVSSGGVTLQCOTRYGF 120

QY 121 DQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRCYSFSSRDPYLSAPSDPLEL 180
Db 121 DQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRCYSFSSRDPYLSAPSDPLEL 180

QY 181 VVTGTSVTPSRSLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSPKESDSPAGP 240
Db 181 VVTGTSVTPSRSLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRITTSPKESDSPAGP 240

QY 241 ARQYTTKGN 249
Db 241 ARQYTTKGN 249

RESULT 4
US-10-333-481-13
; Sequence 13, Application US/10333481
; Publication No. US20040072256A1
; GENERAL INFORMATION:
; APPLICANT: Ofer Mandelboim
; APPLICANT: Angel Porgador
; TITLE OF INVENTION: NK CELLS ACTIVATING RECEPTORS AND THEIR THERAPEUTIC AND DIAGNOSTIC
; FILE REFERENCE: 68657
; CURRENT APPLICATION NUMBER: US/10/333,481
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: PCT/IL01/00664
; PRIOR FILING DATE: 2001-07-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 13
; LENGTH: 237
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-333-481-13

Query Match 27.3%; Score 355.5; DB 15; Length 237;
Best Local Similarity 38.4%; Pred. No. 3.1e-20;
Matches 81; Conservative 30; Mismatches 77; Indels 23; Gaps 3;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVDLRLKLSRRYQDQAVLFIPAMKR 45
Db 22 QQQTLPKPFIAEHPHVPKQVTCQNGYGAVEYQLHFEGLFAVDRPKPDERINKV 81

QY 46 RYQDQAVLFIPAMKRSLAGRYCSYQNGSLWSPSDQLELVATGVFAKPSLSAQPGPAVS 105
Db 82 KF-----YIPDMNSRMAGQYSCIYRVGELWSEPSNLLDLVVTWMTYDTPTLVHPGPEVI 135

QY 106 SGGDVTLQCOTRYGDFQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRCYSFSS 165
Db 136 SGEKVTFFYCRDLDTATSMFLLLKEGRSSHVQRGYGVQAEFFPLGPVTTAHRGTYRC--PGS 193

QY 166 RDPYLSAPSDPLELVVVTGTSVTPSRSLPTEP 196
Db 194 YNNHAWSPFPSEPVKLLVTGDIENSTSLAPEDP 224

RESULT 5
US-10-450-763-40516
; Sequence 40516, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 40516
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (3)..(39)
; OTHER INFORMATION: RECEPTOR CELL NK GLYCOPROTEIN IMMUNOGLOB domain identified by
; OTHER INFORMATION: eMATRIX, accession number PD01652A, p-value=1.000e-40, raw score
; OTHER INFORMATION: of 15.35
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (42)..(147)
; OTHER INFORMATION: Immunoglobulin domain identified by PFam, accession name ig,
; OTHER INFORMATION: E-value=3.9e-05, PFam score of 21.6
US-10-450-763-40516

Query Match 21.4%; Score 279.5; DB 18; Length 170;
Best Local Similarity 37.7%; Pred. No. 2.3e-14;
Matches 72; Conservative 22; Mismatches 56; Indels 41; Gaps 7;

QY 7 KPSLQALPSSLVPLEKPVTLRCQPPGVDLRLKLSRRYQDQAVLFIPAMKRSLAGRY 66
Db 7 KPSFLALPGHLVKSEETVILQCWSDVMFEHLLHR-----EGTY 45

QY 67 RC-----SYQNGSLWSPSDQLELVATGVFAKPSLSAQPGPAVSSGGVTLQCOTRYG 119
Db 46 RCYGSVPHSPYQ----LSAPSDPLDMVIIGLYEKPSLSAQPGTVQAGENVTLSCSRSS 101

QY 120 FDQFALYKEGDPAPYKNP-----ERWYRASFPFIITVTAHSGTYRCYSFSSRD-PYLWSA 173
Db 102 YDMYHLSRGEAHERRLPAVRISINGTFAQDFPL--GPATHGGTYRCFG-SFRDAPYEWSN 158

QY 174 PSDPLELVVTG 184
Db 159 SSDPLLVSVTG 169

RESULT 6
US-10-446-826-2
; Sequence 2, Application US/10446826
; Publication No. US20030186885A1
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI

```
; APPLICANT: YAMAMOTO, NAOHASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
; FILE REFERENCE: 03459.0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-826-2

Query Match      20.9%; Score 272; DB 14; Length 74;
Best Local Similarity 98.1%; Pred. No. 3.3e-14;
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSSSRYQDQAVLF 54
      |||||||
Db      21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSSSRYHDQAVLF 74

RESULT 7
US-10-446-826-3
; Sequence 3, Application US/10446826
; Publication No. US20030186885A1
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOHASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
; FILE REFERENCE: 03459.0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-826-3

Query Match      20.9%; Score 272; DB 14; Length 74;
Best Local Similarity 98.1%; Pred. No. 3.3e-14;
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSSSRYQDQAVLF 54
      |||||||
Db      21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSSSRYHDQAVLF 74

RESULT 8
US-10-446-826-2
; Sequence 2, Application US/10446826
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```
; Publication No. US20040152628A9
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOHASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
; FILE REFERENCE: 03459.0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-826-2

Query Match      20.9%; Score 272; DB 16; Length 74;
Best Local Similarity 98.1%; Pred. No. 3.3e-14;
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSSSRYQDQAVLF 54
      |||||||
Db      21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSSSRYHDQAVLF 74

RESULT 9
US-10-446-826-3
; Sequence 3, Application US/10446826
; Publication No. US20040152628A9
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOHASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
; FILE REFERENCE: 03459.0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-826-3

Query Match      20.9%; Score 272; DB 16; Length 74;
Best Local Similarity 98.1%; Pred. No. 3.3e-14;
Matches 53; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSSSRYQDQAVLF 54
      |||||||
Db      21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSSSRYHDQAVLF 74
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RESULT 10
US-09-832-312-7
; Sequence 7, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-7

Query Match 20.6%; Score 268; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 160
Db 1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47

RESULT 11
US-09-829-495-7
; Sequence 7, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR FILING DATE: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-829-495-7

Query Match 20.6%; Score 268; DB 11; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 160

Db 1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47

RESULT 12
US-10-850-034-7
; Sequence 7, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-850-034-7

Query Match 20.6%; Score 268; DB 16; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.9e-14;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 160
Db 1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47

RESULT 13
US-09-864-761-41304
; Sequence 41304, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667


```

; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-850-034-23

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Query Match      16.9%; Score 220; DB 16; Length 47;
Best Local Similarity 78.7%; Pred. NO. 2.6e-10;
Matches 37: Conservative 4; Mismatches 6; Indels 0; Gaps 0;

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Qy		114	CQTRYGDFQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRC	160
Dd		1	COSPYSFDEFVLYKEGDTGPYKRPEKMYRANFPITVTAAHSGTYRC	47

RESULT 17
US-09-864-761-35700
; Sequence 35700, Application US/09864761
; Patent No. US2002048763A1
; GENERAL INFORMATION:

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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 35700
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009892.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
; OTHER INFORMATION: SWISSPROT HIT: P43626, EVALUAE 2.00e-11
; OTHER INFORMATION: EST_HUMAN HIT: AU120189.1, EVALUAE 2.00e-25
; US-09-864-761-35700

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Query Match	16.6%;	Score 216.5;	DB 9;	Length 100;
Best Local Similarity	50.0%;	Pred. No. 1.3e-09;		
Matches	49;	Conservative 13;	Mismatches 31;	Indels 5;
				Gaps 1;

QY 91 FAKPSLSAQPGPAVSSGGDVTLCQTRYGDFQFALYKEGDPAP-----YKNPERWYRAS F 145

pb 3 YDRPSLSVQRYPTVAPGKNVTLLCOSRGQFHTLLTKEGAGHPPLHLRSEHQAOQNQAEE F 62

QY 146 PIITVTAHSGTTRCYCFSSRRDPYLWSAPSDPLELVVT 183

63 RMGPVYTAHVGTTRCYCFSSLSNPYLLSLPSDELVVS 100

RESULT 18
US-9-864-761-36185
; Sequence 36185, Application US/09864761
; Patent No. US2002048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 03:37:27 ; Search time 39 Seconds
(without alignments)
614.307 Million cell updates/sec

Title: US-09-503-387-3_COPY_21_269
Perfect score: 1304
Sequence: 1 QSGPLPKPSLQALPSSLVPL.....SPKESDSPAGPARQVYTKGN 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 129754

Minimum DB seq length: 0
Maximum DB seq length: 250

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	305	23.4	239	2	G02630 Fc alphaRb - human
2	145	11.1	237	2	A42013 alpha-1-B-glycoprotein
3	141.5	10.9	184	2	T46433 hypothetical protein
4	88.5	6.8	189	2	G70512 probable lppK protein
5	88.5	6.8	233	2	S29577 Ig light chain - r
6	88.5	6.8	235	2	S20000 Ig light chain pre
7	88.5	6.8	246	2	PC4397 mucin 3 T10 - huma
8	87	6.7	236	2	PC4396 mucin 3 T9 - human
9	86	6.6	233	1	JU0284 Fc gamma (IGG) rec
10	82.5	6.3	148	2	D71549 hypothetical protein
11	79.5	6.1	155	2	G72548 hypothetical protein
12	79.5	6.1	243	2	AC3600 cellulase (EC 3.2.
13	79	6.1	213	2	A21177 Ig light chain pre
14	78.5	6.0	136	2	JQ0473 T-cell receptor be
15	78	6.0	206	2	A40305 biliary glycoprotein
16	78	6.0	238	2	T40820 proline-rich protein
17	76.5	5.9	138	2	E75509 hypothetical protein
18	76.5	5.9	233	2	JH0372 Ig gamma chain (WM
19	75.5	5.8	178	2	S29594 mucin - rhesus mac
20	75.5	5.8	216	2	I51920 hypothetical 26K p
21	75.5	5.8	226	2	JQ1263 neu differentiation
22	75.5	5.8	230	2	A56210 protein T2211.8 [
23	75.5	5.8	233	2	A86344 mucin like protein
24	75	5.8	235	2	S25755 Ig lambda chain -
25	75	5.8	243	2	S25755 Ig kappa chain - m
26	74.5	5.7	235	2	S25058 leukocyte common a
27	74	5.7	183	2	A28335 heregulin precursor
28	74	5.7	241	2	D43273 elongation factor
29	73.5	5.6	186	2	H97920

30	73.5	5.6	186	2	D95050 translation elonga
31	73.5	5.6	243	2	B41710 promastigote surfa
32	73	5.6	85	2	B35690 mucin 3 (clone SIB
33	73	5.6	136	2	S16848 Ig lambda chain V-
34	73	5.6	166	2	A33402 pregnancy-specif
35	73	5.6	182	2	I83053 pregnancy-specif
36	73	5.6	201	1	WMBEHL UL4 protein - huma
37	73	5.6	235	2	S14675 Ig lambda chain -
38	72.5	5.6	210	2	JC4122 pregnancy-specif
39	72.5	5.6	215	2	B48463 Ras-like GTP-bind
40	72.5	5.6	244	2	T12458 hypothetical prote
41	72	5.5	182	2	A34647 pregnancy-specif
42	72	5.5	212	2	PN0565 iduronate-2-sulfat
43	72	5.5	229	2	H83425 probable enoyl-CoA
44	72	5.5	233	2	S25747 Ig lambda chain -
45	72	5.5	241	2	S32359 glial growth facto
46	71.5	5.5	148	2	S35788 hypothetical prote
47	71.5	5.5	194	2	E95375 probable acetyltra
48	71.5	5.5	232	2	S17399 Ig lambda chain pr
49	71.5	5.5	239	2	T45806 hypothetical prote
50	71	5.4	160	2	I47163 cytolitic trigger
51	71	5.4	206	2	A75493 hypothetical prote
52	71	5.4	215	2	T23195 hypothetical prote
53	71	5.4	230	2	S49449 Ig lambda chain -
54	71	5.4	240	2	A39016 T-cell surface gly
55	70.5	5.4	109	1	KVRB37 Ig kappa chain V r
56	70.5	5.4	201	2	A97776 recombination prot
57	70.5	5.4	245	2	S19018 complement subcomp
58	70	5.4	119	2	S30526 Ig lambda chain V
59	70	5.4	136	2	S42610 ARMVlambda protein
60	70	5.4	204	2	S22639 alpha-amylase/subt
61	70	5.4	235	2	S25758 Ig lambda chain -
62	69.5	5.3	215	2	A48463 Ras-like GTP-bind
63	69	5.3	152	2	B26471 Ig heavy chain pre
64	69	5.3	153	2	F96725 hypothetical prote
65	69	5.3	160	2	A72541 hypothetical prote
66	69	5.3	206	2	T23852 hypothetical prote
67	69	5.3	240	2	S01299 OX-45 membrane gly
68	68.5	5.3	179	2	S34345 hypothetical prote
69	68.5	5.3	221	2	S49220 Ig gamma-1 chain -
70	68.5	5.3	242	2	S06942 hypothetical prote
71	68.5	5.3	248	2	AH0472 probable chaperone
72	68	5.2	139	2	S36325 T-cell receptor de
73	68	5.2	212	2	C33258 pregnancy-specif
74	68	5.2	240	2	A36791 hypothetical prote
75	67.5	5.2	104	2	I47165 cytolitic trigger
76	67.5	5.2	116	2	F30517 Ig heavy chain pre
77	67.5	5.2	128	2	A35690 mucin 3 (clone SIB
78	67.5	5.2	238	2	S66358 DNA-binding protei
79	67.5	5.2	240	2	A41797 Ig light chain - s
80	67	5.1	140	2	I76667 pregnancy-specif
81	67	5.1	180	2	D72629 hypothetical prote
82	67	5.1	183	2	A12274 GTP-binding nuclea
83	67	5.1	213	2	A99104 Ig lambda chain -
84	67	5.1	231	2	S25738 hypothetical prote
85	66.5	5.1	153	2	S67294 conserved hypothet
86	66.5	5.1	197	2	B81720 hypothetical prote
87	66.5	5.1	216	2	T15317 NAC domain-like pr
88	66.5	5.1	228	2	T47425 Ig lambda chain -
89	66.5	5.1	232	2	S25756 Ig kappa chain pre
90	66.5	5.1	234	2	S01320 carcinoembryonic a
91	66	5.1	119	2	B33876 T-cell receptor be
92	66	5.1	135	2	JQ0472 Ig light chain - r
93	66	5.1	167	2	E75541 MutT/nudix family
94	66	5.1	192	2	S29579 Damx-related prote
95	66	5.1	195	2	B82443 hypothetical prote
96	66	5.1	226	2	T29210 Ig light chain - r
97	66	5.1	228	2	S29575 Ig lambda chain -
98	66	5.1	235	2	S25759 hypothetical prote
99	65.5	5.0	181	2	T48558 penicillin-binding
100	65.5	5.0	188	2	S31952

ALIGNMENTS

RESULT 1
G02630
FcalphaRb - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02630
R;van Dijk, T.B.; Morton, H.C.; Caldenhoven, E.; Bracke, M.; Raaijmakers, J.A.M.; Lammer
submitted to the EMBL Data Library, April 1996
A;Reference number: H01508
A;Accession: G02630
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-239 <VAN>
A;Cross-references: UNIPROT:P24071; EMBL:U56236; NID:gl326228; PID:gl326229

Query Match 23.4%; Score 305; DB 2; Length 239;
Best Local Similarity 36.7%; Pred. No. 9.3e-17;
Matches 72; Conservative 34; Mismatches 78; Indels 12; Gaps 2;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQPPGVVDLYRLEKLSRSSRYQD----- 49
DB 22 QEGDFPMPFISAKSSPVIPLDGSVKIQCAIREAYLTQLMIKNSTYREIGRRLKFWNET 81

QY 50 QAVLFIPAMKRSLAGRYCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGD 109
DB 82 DPEFVIDHMDANKAGRYCQYRIGHYRFYSDTLELVVTLGYKPFLSADRGLVLMGEN 141

QY 110 VTLQCQTRY-GFDQFALYKEGDPAPYKKNPERWYRASFPITVTAAHSGTYRCYSFSSRDP 168
DB 142 ISLTCSSAHIPDFRFLAKEGELSLPQHQSGEHPANFSLGPVDLNVSGIYRCYGNRSP 201

QY 169 YLWSAPSDPLELVVTG 184
DB 202 YLWSFPSNALELVVTG 217

RESULT 2
A42013
alpha-1-B-glycoprotein - North American opossum (fragments)
C;Species: Didelphis virginiana, Didelphis marsupialis virginiana (North American opossu
C;Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
C;Accession: A42013
R;Catanesi, J.J.; Kress, L.F.
Biochemistry 31, 410-418, 1992
A;Title: Isolation from opossum serum of a metalloproteinase inhibitor homologous to hum
A;Reference number: A42013; MUID:92118834; PMID:1731898
A;Accession: A42013
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-237 <CAT>
A;Cross-references: UNIPROT:Q28359; GB:J05356
C;Keywords: glycoprotein

Query Match 11.1%; Score 145; DB 2; Length 237;
Best Local Similarity 29.4%; Pred. No. 0.00032;
Matches 58; Conservative 25; Mismatches 92; Indels 22; Gaps 10;

QY 4 PLPKPSLQALPSSLVPLEKPVTLRCQGP-PGV--DLYR---LEKLSRSRYQDQAVLFIPA 57
DB 43 PLPAPSLRAEPGGPWILRGVETKLHCRGVLLGMIFDLYGEQEPEVKSSHTPGTEATFIV- 101

QY 58 MKRSLAGRYCSYQ-----NGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTIQ 113
DB 102 ---NSTGNYSCLYRAPAPAPSVNSTPSETIHVVIPDFLPAKFYILNNRVFRPGDIVTVS 158

QY 114 CQTRYG----FD-QFALYKEGDPAPYK--NPERWYRASFPITVTAAHSGTYRC-YSFSSR 166
DB 159 CQARFSEREYDLEFLFKDGGQETLVEVVLTSDQMKVFFDLTAVGPEDEGKYSERYFRNG 218

QY 167 DPYLWSAPSDPLELVVT 183

Db 219 PP-IWSEDSNILELVVT 234

RESULT 3
T46433
hypothetical protein DKFZp434F0326.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46433
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23028
A;Accession: T46433
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-184 <AAA>
A;Cross-references: UNIPROT:Q9NTC8; EMBL:AL137369
A;Experimental source: adult testis; clone DKFZp434F0326
C;Genetics:
A;Note: DKFZp434F0326.1

Query Match 10.9%; Score 141.5; DB 2; Length 184;
Best Local Similarity 38.8%; Pred. No. 0.00045;
Matches 38; Conservative 8; Mismatches 49; Indels 3; Gaps 1;

QY 84 ELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGFDQFALYKEGDPAPYKKNPERWYRA 143
DB 1 EIWTDKPPKPSLSAWPSTMFKLGDITLQCRGPLPGVEFVLEHGEAPQQFSE---DG 57

QY 144 SFPITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELV 181
DB 58 DFVINNVEGKGIGNYSCSYRLQAYPDIWSEPSDPLELV 95

RESULT 4
G70512
probable lppK protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: G70512
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: G70512
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-189 <COL>
A;Cross-references: UNIPROT:Q33251; GB:Z97559; GB:AL123456; NID:g3261820; PIDN:CAB10707.1
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: lppK

Query Match 6.8%; Score 88.5; DB 2; Length 189;
Best Local Similarity 25.1%; Pred. No. 6.6;
Matches 47; Conservative 24; Mismatches 81; Indels 35; Gaps 8;

QY 68 CSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGFDQFALYK 127
DB 23 CSHPEFKRSSPPAPSLPPVTSSPLEAAPIITPLPAPEALI--DV-----LSR 66

QY 128 EGDPA-PYKKNPERWYRASFPIT-----VTAHSGTYRCYSFSSRDPYLWS--APSDPL 178
DB 67 LADPAVPGTNKVQLIEGATPENAAALDRFTTALRDGSLYLPMTFAAND-IAWSDNKPSDVM 125

QY 179 ELVVTTGTSVTPSRLTEPPSSVA-----EFSEATAELTVSFTNKVFTTETSRITTSPE 233
DB 126 ATVVVTTAHPDNRREFTFMFEVSVFKGWQLSRQTAEMLLAMGNSPDSTPSA----TSPAP 181

QY 234 SDSPAGP 240
Db 182 APSPTPP 188

RESULT 5
S29577
Ig light chain - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
C:Accession: I51043; S29577
R:Daggfeldt, A.; Bengten, E.; Pilstrom, L.
Immunogenetics 38, 199-209, 1993
A:Title: A cluster type organization of the loci of the immunoglobulin light chain in Atlantic salmon
of cDNAs and hybridization analysis.
A:Reference number: I50732; MUID:93279739; PMID:8505063
A:Accession: I51043
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <DA2>
A:Cross-references: EMBL:X68519; NID:g64175; PIDN:CAA48530.1; PID:g64176
C:Genetics:
A:Gene: IGL
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 6.8%; Score 88.5; DB 2; Length 233;
Best Local Similarity 25.3%; Pred. No. 8.5;
Matches 41; Conservative 22; Mismatches 66; Indels 33; Gaps 7;

QY 103 AVSSGGDVTLOQT-----RY-----GFDQFALY-----KEGDPAPYKNPE 138
Db 27 AVSVGHVSLSCKTSSAVYSDGNHLYWYQKPGAPKLLIYWAKTLQSGTSPSRFSGSG 86

QY 139 RMYRASFPITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSTVTPSRLPTEPPS 198
Db 87 SGSDFTLTISGQAEDTGDIYQSFHSGPVYTFGSGT-----RLDVGSNSAPT-LTVLPSPS 141

QY 199 SVAEFSEATAELTVSFTNKVFTTETS---RSITTSPKESDSP 237
Db 142 S-EELSSITTTATLMLANKGFPDSDWTIRWKVDGTSQKQEASP 182

RESULT 6
S20000
Ig light chain precursor - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20000; S29580
R:Daggfeldt, A.; Bengten, E.; Pilstrom, L.
submitted to the EMBL Data Library, March 1992
A:Reference number: S20000
A:Accession: S20000
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-235 <DAG>
A:Cross-references: EMBL:X65260; NID:g64181; PID:g64182
R:Daggfeldt, A.; Bengten, E.; Pilstrom, L.
submitted to the EMBL Data Library, September 1992
A:Description: A cluster type organisation of the loci of the immunoglobulin light chain
A:Reference number: S29569
A:Accession: S29580
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 122-133 <DA2>
A:Cross-references: EMBL:X68522; NID:g64180; PID:g938274
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:38-115/Domain: immunoglobulin homology <IMM>

Query Match 6.8%; Score 88.5; DB 2; Length 235;
Best Local Similarity 23.8%; Pred. No. 8.6;
Matches 57; Conservative 24; Mismatches 73; Indels 85; Gaps 13;

QY 24 VTLRCQ-----GPPGVDLR-----LEKLSRRYQDOA-----VLFI 55
Db 41 VTLRCRFNKPPACSPPCVAVYQKPGAPQLLIYYATTLOSGTSPSRFSGSGSDFTLTI 100

QY 56 PAMKRSLAGRYRC-SYQNGSLWSLPS-DQLELVATGVFAKPSLSAQP--GPAVSSGGDVT 111
Db 101 SGVQAEADAGDIYQCQSYHSGDVWTFGSGTRLDV---GSNSAPTTLVLPSPSEELSTTTAT 157

QY 112 LQCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSFSSR----- 166
Db 158 LTCLANKGF-----PSDW-----TIRWKVDGPSQKQGTSSRVLEKD 193

QY 167 DPYLWSAPSDPLELVVTGTSTVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSR 225
Db 194 GLYSWSS-----TLTLTGLEWTKA-----GEVTCQAQNSQTS---VTKTLR 231

RESULT 7
PC4397
mucin 3 T10 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1997 #sequence_revision 10-Nov-1997 #text_change 09-Jul-2004
C:Accession: PC4397
R:Van Klinken, B.J.W.; Van Dijken, T.C.; Oussoren, E.; Bueller, H.A.; Dekker, J.; Einerha
Biochem. Biophys. Res. Commun. 238, 143-148, 1997
A:Title: Molecular cloning of human MUC3 cDNA reveals a novel 59 amino acid tandem repeat
A:Reference number: PC4395; MUID:97445141; PMID:9299468
A:Accession: PC4397
A:Molecule type: mRNA
A:Residues: 1-246 <VAN>
A:Cross-references: UNIPROT:O14762; DDBJ:AF016694; NID:g2454618; PIDN:AAB71687.1; PID:g24
A:Experimental source: intestine
F:1-46,47-105,106-164,165-223,224-246/Region: repeat

Query Match 6.8%; Score 88.5; DB 2; Length 246;
Best Local Similarity 25.3%; Pred. No. 9.1;
Matches 46; Conservative 19; Mismatches 68; Indels 49; Gaps 6;

QY 69 SYQNGSLWSLPSDQLELVATGVFAKPSLSAQP GPAVSSGGDVT LQCQTRYGFDQFALYKE 128
Db 54 SSETSTLTSTPADTSTPTVTYSQASSSPPTADGTSMT-----STYSE 96

QY 129 GDPAPYKNPERWYRASFPITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVT 188
Db 97 GGTP-----LTSVPVSTTPV-----SSEASTLSTTPVDSSSPVVTSTEGT 137

QY 189 PSRLPTEPPS-SVAEFSEATAELT-----VSFTNKVFTT--ETSRITTSPKESD 235
Db 138 SSLTPTEGTSIATSTPSEGTPPLTSMPPVSTTTVASSETNSLSLTPADTRTAVTTPQASS 197

QY 236 SP 237
Db 198 TP 199

RESULT 8
PC4396
mucin 3 T9 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 10-Nov-1997 #sequence_revision 10-Nov-1997 #text_change 09-Jul-2004
C:Accession: PC4396
R:Van Klinken, B.J.W.; Van Dijken, T.C.; Oussoren, E.; Bueller, H.A.; Dekker, J.; Einerha
Biochem. Biophys. Res. Commun. 238, 143-148, 1997
A:Title: Molecular cloning of human MUC3 cDNA reveals a novel 59 amino acid tandem repeat
A:Reference number: PC4395; MUID:97445141; PMID:9299468
A:Accession: PC4396
A:Molecule type: mRNA
A:Residues: 1-236 <VAN>
A:Cross-references: UNIPROT:O14761; DDBJ:AF016693; NID:g2454616; PIDN:AAB71686.1; PID:g24
A:Experimental source: intestine
F:1-56,57-115,116-174,175-233,234-236/Region: repeat

```

Query Match          6.7%; Score 87; DB 2; Length 236;
Best Local Similarity 26.0%; Pred. No. 11;
Matches 51; Conservative 27; Mismatches 76; Indels 42; Gaps 10;

QY    75 LWSLPDQLLELV---ATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYGFDFQFALYKEGDP 131
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     52 LTSIPVSTTPVVSSEASTLSATPVDTSTPG---TTSAEATSSPTTAEGIS----IPTSTP 104

QY    132 APYKNPERMYRASFPPIITVTAHSGTYRCYSFSRRDPYLWASAPSDPLELVTGTSTVPGR 191
      ::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     105 SEGKTPLK-----SIPVSNTPVA-----NSEASTLSTTPADNSPPVVTSTAVSSSP 150

QY    192 LPTEPP-----SSVAEFSEAEELTVSFT-----NKVFTE--TSRSITTSPKESDSA 238
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     151 TPAEGTSTAISTPSEGSTALTIPVSTTTVASSEINSLSTPAVTSTPVTTSQAASSSPT 210

QY    239 ---GPARQ---YYTKGN 249
      |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db     211 TADGTSMQTSTYSEGS 226


RESULT 9
JU0284
Fc gamma (IgC) receptor III-B precursor (neutrophil) - human
N:Alternate names: FcR III; IgG Fc receptor precursor, type III-1 (polymorphonuclear gra
C:Species: Homo sapiens (man)
C>Date: 07-Sep-1990 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: JU0284; S00758; I37628; B32933; A31460
R:Ravetch, J.V.; Perussia, B.
J. Exp. Med. 170, 481-497, 1989
A:Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells
A:Reference number: JL0107; MUID:89328325; PMID:2526846
A:Accession: JU0284
A:Molecule type: mRNA
A:Residues: 1-201,'SF',204-233 <RAV>
A:Cross-references: UNIPROT:O75015; GB:J04162
A>Note: The sequence of the receptor from human NK cells, reported in the same paper, di
rboxyl end
R:Simmons, D.; Seed, B.
Nature 333, 568-570, 1988
A:Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane
A:Reference number: S00758; MUID:88232937; PMID:2967436
A:Accession: S00758
A:Molecule type: mRNA
A:Residues: 1-233 <SIM>
A:Cross-references: EMBL:X07934; NID:g29744; PIDN:CAA30758.1; PID:g29745
R:Gessner, J.E.; Grussenmeyer, T.; Kolanus, W.; Schmidt, R.E.
J. Biol. Chem. 270, 1350-1361, 1995
A:Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole
A:Reference number: A55439; MUID:95138131; PMID:7836402
A:Accession: I37628
A:Molecule type: DNA
A:Residues: 1-72 <RES>
A:Cross-references: EMBL:Z46223; NID:g559446; PIDN:CAA86296.1; PID:g871306
R:Scallan, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.Q.
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
A:Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phosp
A:Reference number: A32933; MUID:89296947; PMID:2525780
A:Accession: B32933
A:Molecule type: mRNA
A:Residues: 1-121,'E',123-150,'S',152-233 <SCA>
A:Cross-references: GB:N24854; NID:g184851; PIDN:AAA53507.1; PID:g306930
R:Peltz, G.A.; Grundy, H.O.; Lebo, R.V.; Yssel, H.; Barsh, G.S.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 1013-1017, 1989
A:Title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal
A:Reference number: A31460; MUID:89128838; PMID:2521732
A:Accession: A31460
A:Molecule type: mRNA
A:Residues: 1-35,'R',37-64,'N',66-81,'D',83-105,'V',107-233 <PEL>
A:Cross-references: GB:J04162; NID:g183036; PIDN:AAA35881.1; PID:g183037
C:Comment: This low affinity IgG Fc receptor of neutrophils, which is the product of the
1, yet this receptor lacks 21 residues at the carboxyl end because of an early stop cod
CiGenetics:

```

[illegible]

Query Match 5.9%; Score 76.5; DB 2; Length 233;
Best Local Similarity 25.0%; Pred. No. 74;
Matches 52; Conservative 34; Mismatches 71; Indels 51; Gaps 14;
QY 8 PSLOALPSSILVLEKPVTLRC-----QGPPGVLDLYRLEKLSRRYQDQAVL----- 53
Db PVLRLNSSEF---SDLLKCTTKVDPNKPASELF-----YSFYKDNHIIQNRSHNPLF 73
QY 54 FIPAMKRSIACRYRC--SYQNGSLWSLPSDQLELVATGVFAKPSLSAQ-PGPAVSSGGDV 110
Db FISEANEENSLYQCVVDKGTI-QKKSVDLIDIDLCTSVSQPVLTQHEATNLAEGDKV 132
QY 111 TLQCQTRYGF--DQFALYKEG-----PAPYKNPERWYRASFPPIITVTAHSG-TYRCYS 162
Db KFLCETQLGSLPILYSFYMDGEILGEPLAPSG-----RAASLLISVKAENSGKNYSQCA 186
QY 163 FS--SRDPYLSAPSDP--LELVVTGTS 186
Db ENKVSRD-----ISEPKKFLVVSQTA 208
RESULT 19
S29594
Ig gamma chain (WM65) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: S29594
R;Seymour, R.
submitted to the EMBL Data Library, February 1991
A;Reference number: S29593
A;Accession: S29594
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-178 <SEV>
A;Cross-references: EMBL:X57857; NID:g52590; PIDN:CAA40992.1; PID:g52591
C;Keywords: immunoglobulin
Query Match 5.8%; Score 75.5; DB 2; Length 178;
Best Local Similarity 26.5%; Pred. No. 64;
Matches 36; Conservative 16; Mismatches 63; Indels 21; Gaps 5;
QY 83 LELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYGDFQFALY-----KEG----- 129
Db LMAVVTGVNSEVQLQOSGAELVKPGASVKLSC-TASGFNIKDTYMHVWKQRPKQGLEWIG 62
QY 130 --DPA-PYKNPERWYRASFPPIITVTAHSGTYRCYSFSSRDPYLSAPSD-----PLELVV 182
Db RIDPANGYTEYDPKFGQKATITADTSTNTAYLQSLTSEDYAVYCTGGNYAYGMDYWG 122
QY 183 TGTSVTPSRLPTEPPS 198
Db QGTSVTVSSAKTTPPS 138
RESULT 20
I51920
mucin - rhesus macaque (fragment)
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I51920
R;An, G.; Luo, G.; Wu, R.
Am. J. Respir. Cell Mol. Biol. 10, 546-551, 1994
A;Title: Expression of MUC2 gene is down-regulated by vitamin A at the transcriptional l
A;Reference number: I51920; MUID:94235322; PMID:8179918
A;Accession: I51920
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-216 <RES>
A;Cross-references: UNIPROT:Q28501; EMBL:U00483; NID:g437054; PIDN:AAA20963.1; PID:g4370
C;Genetics:
A;Gene: MUC2

Query Match 5.8%; Score 75.5; DB 2; Length 216;
Best Local Similarity 27.6%; Pred. No. 81;
Matches 29; Conservative 15; Mismatches 40; Indels 21; Gaps 5;
QY 144 SPPIITVTAHSGTYRCYSFSSRDPYLSAPSDPLELVVTGTSVTPSRLP--TEPPSSVA 201
Db STPIITTTTTHPT-----PTPTSTQTPPT-PTPIITTTTTPPTPTPTSTQTPPTP 125
QY 202 EFSEATAELTVSFT-----NKVFTTTSRISITTSKESDSP 237
Db ITSNTTA-WTPPTPTSTQTPPTVPIITTTTATPTPTPTSTQTP 169
RESULT 21
JQ1263
hypothetical 26K protein - foxtail mosaic virus
C;Species: foxtail mosaic virus
C;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 18-Jun-1993
C;Accession: JQ1263
R;Bancroft, J.B.; Rouleau, M.; Johnston, R.; Prins, L.; Mackie, G.A.
J. Gen. Virol. 72, 2173-2181, 1991
A;Title: The entire nucleotide sequence of foxtail mosaic virus RNA.
A;Reference number: JQ1258; MUID:91374015; PMID:1840610
A;Accession: JQ1263
A;Molecule type: genomic RNA
A;Residues: 1-226 <BAN>
A;Cross-references: GB:M62730
Query Match 5.8%; Score 75.5; DB 2; Length 226;
Best Local Similarity 23.7%; Pred. No. 86;
Matches 36; Conservative 19; Mismatches 44; Indels 53; Gaps 8;
QY 14 PSSLVLEKPVTLRCQGP-----GVDLYRLEKLSRRYQDQAVLFIPAMKRSIACRYRCS 69
Db PSN---ISKPTRHCSGQPSRRGSGHLRRRTTGQNSRPRD---LWVTCFSGRTSGRW-CS 77
QY 70 YQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYGDFQFALYKEG 129
Db QMS-----PSNLTQ-----SSGGHVQMRCK-----RPT 100
QY 130 DPAPYKNPERWYRASFPPIITVT-----AAHSG 156
Db SPSPYTRSRTEFFGNHPTLTGTCNCRFSSSHSG 132
RESULT 22
A56210
neu differentiation factor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 08-Sep-2002
C;Accession: A56210
R;Wen, D.; Suggs, S.V.; Karunakaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.;
Mol. Cell. Biol. 14, 1909-1919, 1994
A;Title: Structural and functional aspects of the multiplicity of Neu differentiation fa
A;Reference number: A56210; MUID:94158863; PMID:7509448
A;Accession: A56210
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-230 <RES>
A;Cross-references: EMBL:U02315; NID:g408380; PIDN:AAA19940.1; PID:g408381
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
Query Match 5.8%; Score 75.5; DB 2; Length 230;
Best Local Similarity 24.0%; Pred. No. 88;
Matches 41; Conservative 21; Mismatches 80; Indels 29; Gaps 7;
QY 89 GVFAKPS-LSAQPGPAV-----SSGGDVTLQCQT--RYGFDQFALYKEGDPAP 133
Db GSRGKPGPAEGDPPALPPRLKEMKMSQESAAGSKLVLRCTSESSEYSSSLRFKFKNGNELN 67
QY 134 YKN-PE-----RWYRASFPPIITVTAHSGTYRCYSFSSRDPYLSAPSDPLELVVTGTS 186
Db RKNKPNIKIQKPKGKSELNRINKASLADSGEYMKVISKLG-----DSASANITIVESNEF 124

Qy	187	VTPSRLPTE-----PPSSVAEFSEATAELTVSFTNKVFTTETSRSIITTSPE	233
Db	125	ITGMPASTETAYVSSSPIRISVSTEGANTSSSTSTSTGTSHLIKAEKE	175
RESULT 23			
A86344			
protein T22111.8 [imported] - Arabidopsis thaliana			
C;Species: Arabidopsis thaliana (mouse-ear cress)			
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004			
C;Accession: A86344			
R;Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,			
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;			
ansen, N.F.; Hughes, B.; Huizar, L.			
Nature 408, 816-820, 2000			
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.			
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzialli,			
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.			
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,			
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.			
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.			
A;Reference number: A86141; MUID:21016719; PMID:11130712			
A;Accession: A86344			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-233 <STO>			
A;Cross-references: UNIPROT:Q9LPV4; GB:AE005172; NID:g8886992; PIDN:AAF80652.1; GSPDB:GN			
C;Genetics:			
A;Gene: T22111.8			
A;Map position: 1			
Query Match 5.8%; Score 75.5; DB 2; Length 233;			
Best Local Similarity 21.9%; Pred. No. 89;			
Matches 39; Conservative 27; Mismatches 45; Indels 67; Gaps 11;			
Qy	90	VFAKPSLSAQ-----PGPAVSSGGDVTLCQTRYGFDQFALYKEGD-----	130
Db	22	LFSRPSLSATFLVDGVSVMKSPTVHTGDSVS--KHKGVDLY-IFRNKDAFNVCNFTQA	77
Qy	131	---PAPYKNPERWYRASFPITVTAAHSGTYRCYSFSSRDPYLWSAP-----SDPLELVV	182
Db	78	TLTKPNSSTFTWY-----PSRTGSY-YFSFTNNT---SLPKTCQLNQKLTQVQ	122
Qy	183	TGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRSIITTSPEKSDSPAGP	240
Db	123	ILAAASP---PSQPP-----ATAPVPVS-----EGGVISSPSSYPWPLGP	159
RESULT 24			
PC2022			
mucin like protein Muc2 precursor - rat (fragment)			
C;Species: Rattus norvegicus (Norway rat)			
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 16-Aug-2004			
C;Accession: PC2022			
R;Hansson, G.C.; Baeckstroem, D.; Carlstedt, I.; Klinga-Levan, K.			
Biochem. Biophys. Res. Commun. 198, 181-190, 1994			
A;Title: Molecular cloning of a cDNA coding for a region of an apoprotein from the 'inso			
A;Reference number: PC2022; MUID:94121629; PMID:8292021			
A;Accession: PC2022			
A;Molecule type: mRNA			
A;Residues: 1-235 <HAN>			
A;Cross-references: UNIPROT:Q63349; GB:Z29072; NID:g435534; PIDN:CAA82313.1; PID:g435535			
A;Experimental source: intestine			
C;Genetics:			
A;Gene: muc2			
A;Map position: 1			
C;Superfamily: von Willebrand factor type A repeat homology; von Willebrand factor type			
C;Keywords: glycoprotein			
F;1-53/Region: cysteine-rich			
F;54-235/Region: serine/threonine-rich			
Query Match 5.8%; Score 75; DB 2; Length 235;			

Best Local Similarity 27.5%; Pred. No. 98;			
Matches 33; Conservative 15; Mismatches 48; Indels 24; Gaps 6;			
Qy	135	KNPERWYRASFPITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPT	194
Db	25	KNAEQIGIGGIIPMRMCLNVEINVCCICITS-----TPPSTTTEIQT-TSTTKTSIPT	77
Qy	195	-----EPPSSVAEFSEATA---ELTVSFTNKVFT---TETSRSIITTSPEKSDSPA	238
Db	78	STAMKTPSPSPPTTVTPPETTTTQISTSTSTTTKITTPITETSTPISTT-SQTPSPA	136
RESULT 25			
S25755			
Ig lambda chain - human			
C;Species: Homo sapiens (man)			
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000			
C;Accession: S25755			
R;Combriato, G.; Klobeck, H.G.			
Eur. J. Immunol. 21, 1513-1522, 1991			
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lamt			
A;Reference number: S16439; MUID:91257162; PMID:1904362			
A;Accession: S25755			
A;Status: preliminary; translation not shown			
A;Molecule type: mRNA			
A;Residues: 1-243 <COM>			
A;Cross-references: EMBL:X57820; NID:g33739; PIDN:CAA40957.1; PID:g33740			
C;Superfamily: immunoglobulin V region; immunoglobulin homology			
C;Keywords: heterotetramer; immunoglobulin			
F;158-226/Domain: immunoglobulin homology <IMM>			
Query Match 5.8%; Score 75; DB 2; Length 243;			
Best Local Similarity 23.9%; Pred. No. 1e+02;			
Matches 48; Conservative 25; Mismatches 98; Indels 30; Gaps 8;			
Qy	76	WSPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQTRYGFD-----QFALYKEG	129
Db	3	WTLALLVLLSHCTGSLSQPVLTPQSSHSAASSGASVLTCLMLSSGFVGDFFWIRWYQQKPG	62
Qy	130	DPAPY-----KNPERWYRASFPITVTAAHSGTYRCYSFS---SRDPY--LWSAPS	175
Db	63	NPPRYLLYHSDSNKQGSGVPSRFGSGNDASANAGILRISGLQLEVEADYYCGTWHSNS	122
Qy	176	DPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKV--FTTETSRSIITTSPE	233
Db	123	KNRVFGGGTKLTVLCQPKAAP-SVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKA	181
Qy	234	SDSP--AG-----PARQYYTK	247
Db	182	DSSPVKAGVETTTTPSKQSNK	202

Search completed: October 29, 2005, 03:47:39

Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 03:36:42 ; Search time 172 Seconds
(without alignments)
741.324 Million cell updates/sec

Title: US-09-503-387-3_COPY_21_269
Perfect score: 1304
Sequence: 1 QSGPLPKPSLQALPSSLVPL.....SPKESDSPAGPARQYVTKGN 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 824343

Minimum DB seq length: 0
Maximum DB seq length: 250

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	321	24.6	244	2	Q8MI78 pongo pygma
2	314.5	24.1	193	2	Q6PI73 homo sapien
3	312.5	24.0	239	2	Q9UPI8 homo sapien
4	301.5	23.1	203	2	Q9UNC4 homo sapien
5	296.5	22.7	202	2	O00382 homo sapien
6	292.5	22.4	202	2	O00380 homo sapien
7	291.5	22.4	221	2	Q9UQL7 homo sapien
8	291	22.3	220	2	Q8N741 homo sapien
9	288.5	22.1	203	2	Q9UNB9 homo sapien
10	288.5	22.1	203	2	Q9UNC6 homo sapien
11	287.5	22.0	203	2	Q9UNC0 homo sapien
12	287.5	22.0	203	2	Q9UNC5 homo sapien
13	282.5	21.7	202	2	O00381 homo sapien
14	282.5	21.7	203	2	Q9UNC2 homo sapien
15	279.5	21.4	170	2	Q9UNB7 homo sapien
16	278.5	21.4	203	2	Q9UNC1 homo sapien
17	278.5	21.4	203	2	Q9UNC7 homo sapien
18	276.5	21.2	246	2	Q8MJZ8 macaca mula
19	269.5	20.7	203	2	Q9UNC3 homo sapien
20	259.5	19.9	236	2	Q6QWD6 homo sapien
21	255.5	19.6	235	2	Q6QWD5 homo sapien
22	247.5	19.0	235	2	Q6QWD4 homo sapien
23	245	18.8	174	2	Q8MI79 pongo pygma
24	244.5	18.8	227	2	Q9H7L2 homo sapien
25	238	18.3	151	2	Q99702 homo sapien
26	238	18.3	163	2	Q9UQA2 homo sapien
27	225	17.3	204	2	Q14950 homo sapien
28	224	17.2	247	2	Q8N736 homo sapien
29	223.5	17.1	240	2	Q8MK01 macaca mula
30	217	16.6	245	2	O00547 homo sapien
31	213.5	16.4	209	2	Q92588 homo sapien

32	213.5	16.4	212	2	Q95L80	Q95L80 macaca mula
33	212.5	16.3	157	2	Q8MK14	Q8mk14 macaca mula
34	210.5	16.1	164	2	Q43394	Q43394 homo sapien
35	210.5	16.1	230	2	Q8N738	Q8n738 homo sapien
36	210.5	16.1	241	2	Q8MK22	Q8mk22 macaca mula
37	210	16.1	178	2	Q8MJZ9	Q8mjz9 macaca mula
38	207.5	15.9	247	2	Q8MK24	Q8mk24 macaca mula
39	202.5	15.5	242	2	Q8N6C5	Q8n6c5 homo sapien
40	200.5	15.4	223	2	Q6R4Z5	Q6r4z5 ovis aries
41	200.5	15.4	232	2	Q8NHJ0	Q8nhj0 homo sapien
42	199	15.3	222	2	Q86VI6	Q86vi6 homo sapien
43	197.5	15.1	169	2	Q8MK13	Q8mk13 macaca mula
44	195.5	15.0	239	2	Q6H2G6	Q6h2g6 homo sapien
45	193.5	14.8	119	2	Q8MK00	Q8mk00 macaca mula
46	193.5	14.8	233	2	Q925N5	Q925n5 rattus norv
47	193	14.8	125	2	Q78200	Q78200 homo sapien
48	193	14.8	186	2	Q95L79	Q95l79 macaca mula
49	191.5	14.7	153	2	Q9UNB5	Q9unb5 homo sapien
50	191.5	14.7	178	2	Q92592	Q92592 homo sapien
51	190.5	14.6	232	2	Q8BMN5	Q8bmns mus musculu
52	189.5	14.5	161	2	Q95L78	Q95l78 macaca mula
53	188.5	14.5	243	2	Q92803	Q92803 homo sapien
54	188	14.4	206	2	Q14949	Q14949 homo sapien
55	183.5	14.1	229	2	Q8MK21	Q8mk21 macaca mula
56	170.5	13.1	152	2	Q6ISS4	Q6is84 homo sapien
57	163	12.5	166	2	Q9UNB4	Q9unb4 homo sapien
58	162.5	12.5	105	2	Q9UNB6	Q9unb6 homo sapien
59	160.5	12.3	138	2	Q6QWD7	Q6qwd7 homo sapien
60	160	12.3	152	2	Q6QWD9	Q6qwd9 homo sapien
61	150.5	11.5	105	2	Q9UNB8	Q9unb8 homo sapien
62	147	11.3	143	2	Q86VI5	Q86vi5 homo sapien
63	145	11.1	211	2	Q28359	Q28359 didelphis m
64	144.5	11.1	130	2	Q96L49	Q96l49 homo sapien
65	144.5	11.1	144	2	Q96L47	Q96l47 homo sapien
66	143.5	11.0	109	2	Q96L48	Q96l48 homo sapien
67	142.5	10.9	95	2	Q8NHJ5	Q8nhj5 homo sapien
68	141.5	10.9	184	2	Q9NTC8	Q9ntc8 homo sapien
69	135	10.4	236	2	Q6UX27	Q6ux27 homo sapien
70	126.5	9.7	225	2	Q96PJ1	Q96pj1 homo sapien
71	125.5	9.6	219	2	Q96PJ4	Q96pj4 homo sapien
72	122.5	9.4	246	2	Q9JKL2	Q9jkl2 rattus norv
73	121	9.3	208	2	Q8C233	Q8c233 mus musculu
74	109.5	8.4	179	2	Q92587	Q92587 homo sapien
75	109.5	8.4	205	2	Q92591	Q92591 homo sapien
76	109.5	8.4	217	2	Q92589	Q92589 homo sapien
77	98	7.5	226	2	Q8N440	Q8n440 homo sapien
78	94	7.2	235	2	Q6PIK1	Q6pik1 homo sapien
79	93	7.1	63	2	Q6PEZ4	Q6pez4 homo sapien
80	93	7.1	230	2	Q8C6N8	Q8c6n8 mus musculu
81	92	7.1	64	2	Q75755	Q75755 homo sapien
82	92	7.1	247	2	Q9WUL5	Q9wul5 mus musculu
83	91.5	7.0	236	2	Q90696	Q90696 bovine herp
84	91.5	7.0	243	2	Q39501	Q39501 bovine herp
85	91.5	7.0	248	2	Q9D0T4	Q9d0t4 mus musculu
86	89	6.8	171	2	Q95N20	Q95n20 sus scrofa
87	88.5	6.8	189	1	LPPK_MYCBO	P65301 mycobacteri
88	88.5	6.8	189	1	LPPK_MYCTU	P65300 mycobacteri
89	88.5	6.8	246	2	O14762	O14762 homo sapien
90	87	6.7	236	2	O14761	O14761 homo sapien
91	86.5	6.6	250	2	Q7SEF8	Q7sef8 neurospora
92	86	6.6	233	1	FC3B_HUMAN	Q75015 homo sapien
93	86	6.6	249	2	Q82LM6	Q82lm6 streptomyce
94	86	6.6	250	1	FCG3_BOVIN	P79107 bos taurus
95	85.5	6.6	114	2	Q8H2N0	Q8h2n0 oryza sativ
96	85.5	6.6	127	2	Q9QMB1	Q9qmb1 human immun
97	85.5	6.6	154	2	Q8N733	Q8n733 homo sapien
98	85.5	6.6	224	2	Q7T5F2	Q7t5f2 cercopithec
99	85.5	6.6	243	2	Q806C8	Q806c8 cercopithec
100	82.5	6.3	148	2	O84167	O84167 chlamydia t

ALIGNMENTS


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RESULT 1
Q8MI78
AC Q8MI78 PRELIMINARY; PRT; 244 AA.
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Natural killer cell immunoglobulin-like receptor (Fragment).
GN Name=Popy-KIR2DL4;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22072192; PubMed=12077248;
RA Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
RT "NK cell receptors of the orangutan (Pongo pygmaeus): a pivotal
RT species for tracking the coevolution of killer cell Ig-like receptors
RT with MHC-C.";
RL J. Immunol. 169:220-229(2002).
DR EMBL; AF470389; AAM78489.1; -.
DR HSSP; P43628; 1B6U.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
KW Receptor.
FT NON_TER
SQ SEQUENCE 244 AA; 27269 MW; BF67E2177E659FB6 CRC64;

Query Match 24.6%; Score 321; DB 2; Length 244;
Best Local Similarity 36.2%; Pred. No. 3.8e-17;
Matches 84; Conservative 34; Mismatches 92; Indels 22; Gaps 7;

Qy 7 KPSLOALPSSSLVPLEKPVTLRCQPPGVDLYRLEKLS-----SRYQDQAVLFIPAMK 59
Db 1 KPFCSAWPSAVVPQGGHVTLRCHYRRGNIFTLYKDGVPVPELYNRFWNSFLISP-VT 59
Qy 60 RSLAGRYRC---SYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQQT 116
Db 60 PAHAGTYRCRGFHPHSPTWSAPSPLVIMVTGLYEKPSLSAQPGPTVRAGENVTLCSS 119
Qy 117 RYGFDDQFALYKEGDPAPYKNP-----ERWYRASFPFIITVTAHSGTYRCYSFSSRDPYLW 171
Db 120 WSSFDWMYHLSREGEAHQLRLPAVPSINGTFQADFPL--GPATHRGTYRCFGSFRGSPYEW 177
Qy 172 SAPSDPLELVVGTSTVTPSRLPTEP--PSSVAEFSEFAELTVSFTNKVFTT 221
Db 178 SDPSDPLLVSVTGNPSSWSPSTEPSFTKGIARHLHAVIRYSVAII--LFTT 227

RESULT 2
Q6PI73
AC Q6PI73 PRELIMINARY; PRT; 193 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LILRB2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041708; AAH41708.1; -.
DR HSSP; P43628; 1B6U.
DR InterPro; IPR007110; Ig-like.
SQ SEQUENCE 193 AA; 21175 MW; 6721E1740AC1BDDA CRC64;

Query Match 24.1%; Score 314.5; DB 2; Length 193;
Best Local Similarity 41.4%; Pred. No. 9.1e-17;
Matches 70; Conservative 28; Mismatches 56; Indels 15; Gaps 3;

Qy 1 QSGPLPKPSLOALPSSSLVPLEKPVTLRCQPPGVDLYRLEKLSRRYQD-----QA 51
Db 22 QAGPEPKPTLWAEPSGVISWGSPTIWCQGSLEAQEYQLDKESPEPLDRNPLEPKNKA 81
Qy 52 VLFTPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVT 111
Db 82 RFSIPSMTOHHAGRYRCHYYSAGWSEPSDPLELVMTGFYNKPTLSALPSPVVASGGNMT 141
Qy 112 LQCQTRYGFDQFALYKEGD---PAPYKNPE---RWYRASFPFIITVTAH 154
Db 142 LRCGSKGYHHFVLMKEGHEQLPRTLDSQQLHSGGFQALFPVGPVTPSH 190

RESULT 3
Q9UPI8
ID Q9UPI8 PRELIMINARY; PRT; 239 AA.
AC Q9UPI8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Natural killer associated transcript 2 (Fragment).
GN Name=KIR2DL3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA Danganan L., Erlar A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Attix C., Andreise T., Frankheim M., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006293; AAD03160.1; -.
DR HSSP; P43628; 1B6U.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
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DR SMART; SM00409; IG; 1.
FT NON_TER 239
SQ SEQUENCE 239 AA; 26113 MW; 9AD66A23B4A8F35E CRC64;

Query Match 24.0%; Score 312.5; DB 2; Length 239;
Best Local Similarity 37.4%; Pred. No. 1.7e-16;
Matches 82; Conservative 24; Mismatches 76; Indels 37; Gaps 7;

QY 7 KPSLQALPSSLVPLEKPVTLRCQPPGVLDYRLEKLSRRYQD-----QAVL 53
Db 28 KPSLLAHGPGPLVKSEETVILQCWSDVRFQHFLLHR--EGFKDTHLHIGEHHDGVSKANF 85

QY 54 FIPAMKRSLAGRYRC-----SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSS 106
Db 86 SIGPMQDLAGTRYCYGVSHTSPYQ----LSAPSDPLDIVITGLYEKPSLSAQPGPTVLA 141

QY 107 GGDVTLQCQTRYGFDQFALYKEGD-----PAPYKNPERWYRASFPITVTAHSGTYR 159
Db 142 GESVTLSCSSRSYDMYHLSREGEAHERRFSAKPKVNGT--FQADFPL--GPATHGGTYR 197

QY 160 CYSFSSRDPYLWSAPSDPLELVVTGTSVTPSRRLPTEPPS 198
Db 198 CFGSFRDSPYEWNSSDPLLVSVTGNPSNWPSPTEPSS 236

RESULT 4
Q9UNC4 PRELIMINARY; PRT; 203 AA.
AC Q9UNC4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE P58 killer cell inhibitory receptor KIR-K36 (Fragment).
GN Name=KIR-K36;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors in a single individual."
RL Immunol. Lett. 68:267-274(1999).
DR EMBL; AF135557; AAD48765.1; --
DR HSSP; P43628; 1B6U.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0030110; F:HLA-C specific inhibitory MHC class I recep. . .; NAS.
DR GO; GO:0006952; P:defense response; NAS.
DR GO; GO:0030102; P:negative regulation of natural killer cell . . .; NAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON_TER 203
SQ SEQUENCE 203 AA; 22347 MW; D256BB1EEF4AF122 CRC64;

Query Match 23.1%; Score 301.5; DB 2; Length 203;
Best Local Similarity 38.7%; Pred. No. 1e-15;
Matches 79; Conservative 26; Mismatches 64; Indels 35; Gaps 8;

QY 7 KPSLQALPSSLVPLEKPVTLRCQPPGVLDYRLEKLSRRYQD-----QAVL 53
Db 7 KPSLLAHGPGPLVKSEETVILQCWSDVRFQHFLLHR--EGFKDTHLHIGEHHDGVSKANF 64

QY 54 FIPAMKRSLAGRYRC-----SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSS 106
Db 65 SIGPMQDLAGTRYCYGVSHTSPYQ----LSAPSDPLDIVITGLYEKPSLSAQPGPTVQA 120

QY 107 GGDVTLQCQTRYGFDQFALYKEGDAPYKNP-----ERWYRASFPITVTAHSGTYRCY 161

Db 121 GENVTLCSSRSYDMYHLSREGEAHERRLPAVRSINGTFOADFPL--GPATHGGTYRCF 178

QY 162 SFSSRD-PYLWSAPSDPLELVVTG 184
Db 179 G-SFRDAPYEWNSSDPLLVSVTG 201

RESULT 5
O00382 PRELIMINARY; PRT; 202 AA.
AC O00382;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE P58 NK cell inhibitory receptor NKR-K7 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors in a single individual."
RL Immunol. Lett. 68:267-274(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98018248; PubMed=9378975;
RA Kim J., Chwaee Y.J., Kim M.Y., Choi I.H., Park J.H., Kim S.J.;
RT "Molecular basis of HLA-C recognition by p58 natural killer cell inhibitory receptors."
RL J. Immunol. 159:3875-3882(1997).
DR EMBL; U96190; AAB54120.1; --
DR HSSP; P43628; 1B6U.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 202 AA; 22182 MW; C15D7330639FF82B CRC64;

Query Match 22.7%; Score 296.5; DB 2; Length 202;
Best Local Similarity 37.6%; Pred. No. 2.4e-15;
Matches 77; Conservative 24; Mismatches 67; Indels 37; Gaps 7;

QY 7 KPSLQALPSSLVPLEKPVTLRCQPPGVLDYRLEKLSRRYQD-----QAVL 53
Db 7 KPSLLAHGPGPLVKSEETVILQCWSDVRFQHFLLHR--EGFKDTHLHIGEHHDGISKANF 64

QY 54 FIPAMKRSLAGRYRC-----SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSS 106
Db 65 SIGPMQDLAGTRYCYGVSHTSPYQ----LSAPSDPLDIVITGLYEKPSLSAQPGPTVLA 120

QY 107 GGDVTLQCQTRYGFDQFALYKEGD-----PAPYKNPERWYRASFPITVTAHSGTYR 159
Db 121 GESVTLSCSSRSYDMYHLSREGEAHERRFSAKPKVNGT--FQADFPL--GPATHGGTYR 176

QY 160 CYSFSSRDPYLWSAPSDPLELVVTG 184
Db 177 CFGSFRDSPYEWNSSDPLLVSVTG 201

RESULT 6
O00380 PRELIMINARY; PRT; 202 AA.
AC O00380;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE P50 cell activatory receptor NKR-K1 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;

RA Chwae Y.J., Cho S.E., Kim S.J., Kim J.;

RT "Diversity of the repertoire of p58 killer cell inhibitory receptors in a single individual."

RL Immunol. Lett. 68:267-274(1999).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98018248; PubMed=9378975;

RA Kim J., Chwae Y.J., Kim M.Y., Choi I.H., Park J.H., Kim S.J.;

RT "Molecular basis of HLA-C recognition by p58 natural killer cell inhibitory receptors."

RL J. Immunol. 159:3875-3882(1997).

DR EMBL; U96188; AAB54118.1; -.

DR HSSP; P43628; 1B6U.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 1.

KW Receptor.

FT NON_TER 1

SQ SEQUENCE 202 AA; 2234 MW; 0539C0698D377E86 CRC64;

Query Match 22.4%; Score 292.5; DB 2; Length 202;

Best Local Similarity 39.1%; Pred. No. 5e-15;

Matches 79; Conservative 26; Mismatches 66; Indels 31; Gaps 8;

Qy 7 KPSLQALPSSLVPLEKPVTLRCQGPVGD---LYRLEKLSSSRY-----QDQAVLFI 55

Db 7 KPSFLALPGLVKSEETVILQCWSDMVFHFLLHREGKFNNTLHIGEHHDGVSKANFSI 66

Qy 56 PAMKRSLAGRYRC-----SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGG 108

Db 67 GPMPVLAGTYRCYCGSVPHSPYQ---LSAPSDPLDMVIIGLYEKPSLSAQPGPTVQAGE 122

Qy 109 DVTLCQTRYGFDQFALYKEGDPAPYKNP-----ERWYRASFPPIITVTAHSGTYRCYSF 163

Db 123 NVTLSCSRSSSYDMYHLSREGEAHERRLPAVRSINGTFQADFPL--GPATHGGTYRCFG- 179

Qy 164 SSRD-PYLWSAPSDPLELVVTG 184

Db 180 SFRDAPYEWNSSDPLLVSVTG 201

RESULT 7

Q9UQL7 ID Q9UQL7 PRELIMINARY; PRT; 221 AA.

AC Q9UQL7;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Killer inhibitory receptor 4-1-2 (Fragment).

GN Name=KIR412;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Chae J., Kim Y.M., Ahn J.M., Kim C.G., Kim J., Kim S.J., Park J.H.;

RA Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF134316; AAD24479.1; -.

DR EMBL; AF134312; AAD24479.1; JOINED.

DR EMBL; AF134313; AAD24479.1; JOINED.

DR EMBL; AF134315; AAD24479.1; JOINED.

DR HSSP; P43628; 1B6U.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 1.

KW Receptor.

FT NON_TER 221

SQ SEQUENCE 221 AA; 24291 MW; C4CF5AAD1045FAB4 CRC64;

Query Match 22.4%; Score 291.5; DB 2; Length 221;

Best Local Similarity 37.3%; Pred. No. 6.7e-15;

Matches 76; Conservative 24; Mismatches 67; Indels 37; Gaps 7;

Qy 7 KPSLQALPSSLVPLEKPVTLRCQGPVGDLYRLEKLSSSRYQD-----QAVL 53

Db 28 KPSLLAQPGPLVKSEETVILQCWSDVRFQHFLLHR--EGFKDTLHLIGEHHHDGVSKANF 85

Qy 54 FIPAMKRSLAGRYRC-----SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSS 106

Db 86 SIGPMWQDLAGTYRCYCGSVTHSPYQ---LSAPSDPLDIVITGLYEKPSLSAQPGPTVLA 141

Qy 107 GGDVTLQCQTRYGFDQFALYKEG-----PAPYKNPERWYRASFPPIITVTAHSGTYR 159

Db 142 GESVTLSCSRSSSYDMYHLSREGEAHERRFSAGPKVNGT--FQADFPL--GPATHGGTYR 197

Qy 160 CYSFSSRDPYLWSAPSDPLELVVT 183

Db 198 CFGSFRDSPYEWNSSDPLLVSVT 221

RESULT 8

Q8N741 ID Q8N741 PRELIMINARY; PRT; 220 AA.

AC Q8N741;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE 1060P11.4.7 (Killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4 (Isoform 7) (KIR103-ASD2)).

GN Name=KIR2DL4;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Milne S.;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL133414; CAC40705.1; -.

DR HSSP; P43626; 1NKR.

DR GO; GO:0004872; F:receptor activity; IEA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 1.

KW Receptor.

SQ SEQUENCE 220 AA; 24090 MW; ED70FC9541A39BDE CRC64;

Query Match 22.3%; Score 291; DB 2; Length 220;

Best Local Similarity 36.5%; Pred. No. 7.3e-15;

Matches 72; Conservative 31; Mismatches 76; Indels 18; Gaps 5;

Qy 3 GPLPKPSLQALPSSLVPLEKPVTLRCQGPVGDLYRLEKLS-----SRYQDQAVLFI 55

Db 26 GGQDKPFCSAWPSSAVVPQGGHVTLCRCRRGNIFTLYKKDGVVPVELYNRIFWNSFLIS 85

Qy 56 PAMKRSLAGRYRC---SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTL 112

Db 86 P-VTPAHAGTYRCRGFHPHSPTWAPSPLVIMVTGLYEKPSLTARPGPTVRAGENVTL 144

Qy 113 QCQTRYGFDQFALYKEGDPAPYKNP-----ERWYRASFPPIITVTAHSGTYRCYSFSSRD 167

Db	145	SCSSQSFDIYHLSRGEAHELRLPAVPSINGTFQADPFL--GPATHGETYRCFGSFHGS	202
Qy	168	PYLWSAPSDPLELVVTG 184	
Db	203	PYEWSDPSDPLPVSVTG 219	
RESULT 9			
Q9UNB9	PRELIMINARY; PRT; 203 AA.		
AC	Q9UNB9;		
DT	01-MAY-2000 (TReMBLrel. 13, Created)		
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)		
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)		
DE	p58 killer cell inhibitory receptor KIR-K78 (Fragment).		
GN	Name=KIR-K78;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;		
RA	Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;		
RT	"Diversity of the repertoire of p58 killer cell inhibitory receptors		
RT	in a single individual."		
RL	Immunol. Lett. 68:267-274(1999).		
DR	EMBL; AF135562; AAD48770.1; -.		
DR	HSSP; P43628; 1B6U.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	Pfam; PF00047; ig; 2.		
DR	SMART; SM00409; IG; 1.		
KW	Receptor.		
FT	NON_TER 1		
FT	NON_TER 203		
SQ	SEQUENCE 203 AA; 22256 MW; 91FFF6C166B0C4A8 CRC64;		
Query Match 22.1%; Score 288.5; DB 2; Length 203;			
Best Local Similarity 37.9%; Pred. No. 1e-14;			
Matches 77; Conservative 24; Mismatches 69; Indels 33; Gaps 7;			
Qy	7	KPSLQALPSSLVPLEKPVTLRCQPPGVD---LYRLEKLSRRY-----QDQAVLFI 55	
Db	7	KPSFLALPGLVKSEETVILQCWSDVMFEHFLHREGKFNNTLHLIGEHHGVSKANFSI 66	
Qy	56	PAMKRSLAGRYRC-----SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSG 108	
Db	67	GPMPVLAGTRYRCYGSVPHSPYQ----LSAPSDPLDMVIIIGLYEKPSLSAQPGPTVLAGE 122	
Qy	109	DVTLCQTRYGFDQFALYKEGD-----PAPYKNPERWYRASFPITVTAAHSGTYRCY 161	
Db	123	SVTLSCSSRSSYDMYHLSRGEAHERRFSAGPKVNGT--FQADPFL--GPATHGGTYRCF 178	
Qy	162	SFSSRDPYLWSAPSDPLELVVTG 184	
Db	179	GSFHDSPYEWSKSSDPLLVSVTG 201	
RESULT 10			
Q9UNC6	PRELIMINARY; PRT; 203 AA.		
AC	Q9UNC6;		
DT	01-MAY-2000 (TReMBLrel. 13, Created)		
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)		
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)		
DE	p58 killer cell inhibitory receptor KIR-K9 (Fragment).		
GN	Name=KIR-K9;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		

RN	[1]	SEQUENCE FROM N.A.		
RP		MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;		
RA		Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;		
RT		"Diversity of the repertoire of p58 killer cell inhibitory receptors		
RT		in a single individual.";		
RL		Immunol. Lett. 68:267-274(1999).		
DR		EMBL; AF135555; AAD48763.1; -.		
DR		HSSP; P43626; 1NKR.		
DR		GO; GO:0004872; F:receptor activity; IEA.		
DR		InterPro; IPR003599; Ig.		
DR		InterPro; IPR007110; Ig-like.		
DR		Pfam; PF00047; ig; 2.		
DR		SMART; SM00409; IG; 1.		
KW		Receptor.		
FT		1	1	
FT		203	203	
SQ	SEQUENCE	203 AA; 22299 MW; E5D5CCC37B3EE102 CRC64;		
Query Match 22.1%; Score 288.5; DB 2; Length 203;				
Best Local Similarity 37.6%; Pred. No. 1e-14;				
Matches 77; Conservative 22; Mismatches 69; Indels 37; Gaps 7;				
Qy	7	KPSLQALPSSLVPLEKPVTLRCQPPGVDLYRLEKLSRRYQD-----QAVL 53		
Db	7	KPSLLAHPGRLVKSEETVILQCWSDVMFEHFLHR--EGMFNDTLRLIGEHHGVSKANF 64		
Qy	54	FIPAMKRSLAGRYRC-----SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSS 106		
Db	65	SISRMTQDLAGTRYCYGSVTHSPYQ----VSAPSDPLDIVITGLCEKPSLSAQPGPTVLA 120		
Qy	107	GGDVTLCQTRYGFDQFALYKEGD-----PAPYKNPERWYRASFPITVTAAHSGTYR 159		
Db	121	GESVTLCSSRSSYDMYHLSRGEAHERRFSAGPKVNGT--FQADFP--GPATHGGTYR 176		
Qy	160	CYSFSSRDPYLWSAPSDPLELVVTG 184		
Db	177	CFGSRDPSPYEWSNSSDPLLVSVTG 201		
RESULT 11				
Q9UNC0		PRELIMINARY; PRT; 203 AA.		
ID	Q9UNC0			
AC	Q9UNC0;			
DT	01-MAY-2000 (TReMBLrel. 13, Created)			
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)			
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)			
DE	p58 killer cell inhibitory receptor KIR-K65 (Fragment).			
GN	Name=KIR-K65;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;			
RA	Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;			
RT	"Diversity of the repertoire of p58 killer cell inhibitory receptors			
RT	in a single individual.";			
RL	Immunol. Lett. 68:267-274(1999).			
DR	EMBL; AF135561; AAD48769.1; -.			
DR	HSSP; P43628; 1B6U.			
DR	GO; GO:0005887; C:integral to plasma membrane; NAS.			
DR	GO; GO:0030110; F:HLA-C specific inhibitory MHC class I recep. . .; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	GO; GO:0030102; P:negative regulation of natural killer cell . . .; NAS.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR007110; Ig-like.			
DR	Pfam; PF00047; ig; 2.			
DR	SMART; SM00409; IG; 1.			
KW	Receptor.			
FT		1	1	
FT		203	203	

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual."
RL Immunol. Lett. 68:267-274(1999).
DR EMBL; AF135559; AAD48767.1; -.
DR HSSP; P43626; 1NKR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 203
SQ SEQUENCE 203 AA; 22275 MW; BD27C0F96AC03FAD CRC64;

Query Match 21.7%; Score 282.5; DB 2; Length 203;
Best Local Similarity 37.3%; Pred. No. 3e-14;
Matches 75; Conservative 26; Mismatches 71; Indels 29; Gaps 6;

QY 7 KPSLQALPSSLVPLEKPVTLRCQGGPPGVD---LYRLEKLSRRY-----QDQAVLFI 55
DB 7 KPSFLALPGHLVKSEETVILQCWSDMVFHLLHREGKFNNTLHLIGEHHGVSKANFSI 66

QY 56 PAMKRSAGRYRC-----SYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGG 108
DB 67 GPMPVPLAGTYRCYGVSPHPYQ---LSAPSDPLDMVIIGLYEKPSLSAQLGPTVLAGE 122

QY 109 DVTLCQCTRYGFDQFALYKEGDPAPYKNP-----ERWYRASFPITVTAAHSGTYRCYSF 163
DB 123 NVTLCSSRRSSYDMYHLSREGEAHERRLPAGPKVNGTFQADFPPL--GPATHGGTYRCFGS 180

QY 164 SSRDPYLWSAPSDPLELVVTG 184
DB 181 FHDSPYEWSKSSDPLLVSVTG 201

RESULT 15
Q9UNB7
ID Q9UNB7 PRELIMINARY; PRT; 170 AA.
AC Q9UNB7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE P50 killer cell activating receptor KAR-Kid (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual."
RL Immunol. Lett. 68:267-274(1999).
DR EMBL; AF135564; AAD48758.1; -.
DR HSSP; P43626; 1NKR.
DR GO; GO:0005887; C:integral to plasma membrane; NAS.
DR GO; GO:0030110; F:HLA-C specific inhibitory MHC class I recep. . .; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR GO; GO:0030102; P:negative regulation of natural killer cell . . .; NAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 170
SQ SEQUENCE 170 AA; 18819 MW; 1174C8AEB0115FEA CRC64;

Query Match 21.4%; Score 279.5; DB 2; Length 170;
Best Local Similarity 37.7%; Pred. No. 4.2e-14;
Matches 72; Conservative 22; Mismatches 56; Indels 41; Gaps 7;

QY 7 KPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSRRYQDQAVLFIPAMKRSLAGRY 66
DB 7 KPSFLALPGHLVKSEETVILQCWSDMVFHLLHR-----EGTY 45

QY 67 RC-----SYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYG 119
DB 46 RCYGSVPHSPYQ---LSAPSDPLDMVIIGLYEKPSLSAQPGPTVQAGENVTLSCSSRSS 101

QY 120 FDQFALYKEGDPAPYKNP-----ERWYRASFPITVTAAHSGTYRCYSSSRD-PYLWSA 173
DB 102 YDMYHLSREGEAHERRLPAVRSINGTTFQADFPPL--GPATHGGTYRCFG-SFRDAPYEWSN 158

QY 174 PSDPLELVVTG 184
DB 159 SSDPLLVSVTG 169

RESULT 16
Q9UNCI
ID Q9UNCI PRELIMINARY; PRT; 203 AA.
AC Q9UNCI;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE P58 killer cell inhibitory receptor KIR-K64 (Fragment).
GN Name=KIR-K64;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99351717; PubMed=10424431; DOI=10.1016/S0165-2478(99)00062-0;
RA Chwaee Y.J., Cho S.E., Kim S.J., Kim J.;
RT "Diversity of the repertoire of p58 killer cell inhibitory receptors
in a single individual."
RL Immunol. Lett. 68:267-274(1999).
DR EMBL; AF135560; AAD48768.1; -.
DR HSSP; P43626; 1NKR.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 203
SQ SEQUENCE 203 AA; 22474 MW; 148649A1BF15ED65 CRC64;

Query Match 21.4%; Score 278.5; DB 2; Length 203;
Best Local Similarity 36.0%; Pred. No. 6.2e-14;
Matches 73; Conservative 25; Mismatches 72; Indels 33; Gaps 6;

QY 7 KPSLQALPSSLVPLEKPVTLRCQGGPPGVDLYRLEKLSRRYQD-----QAVL 53
DB 7 KPSFLALPGHLVKSEETVILQCWSDMVFHLLHR--EGMFNDTLRLIGEHHGVSKANF 64

QY 54 FIPAMKRSAGRYRC-----SYQNGSLWSPDQLELVATGVFAKPSLSAQPGPAVSS 106
DB 65 SISRMTQDLAGTYRCYGVSVTHSPYQ---VSAPSDPLDIVIIGLYEKPSLSAQLGPTVLA 120

QY 107 GGDVTLQCCTRYGFDQFALYKEGDPAPYKNP-----ERWYRASFPITVTAAHSGTYRCY 161
DB 121 GENVTLCSSRRSSYDMYHLSREGEAHERRLPAVRSINGTTFQADFPPL--GPATHGGTYRCF 178

QY 162 SFSSRDPYLWSAPSDPLELVVTG 184
DB 179 GSFHDSPEYWSKSSDPLLVSVTG 201


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QY 7 KPSLQALPSSLVBLEKPVTLRCQPPGGVDLYRLKLSRSSRYQDQAV-----LFI 55
Db 7 KPSLLAHPGPLLKSGETVILQCWSDVMFEHFFLHRDGI SEDPSRLVGGQIHDGVSKANFSI 66

QY 56 PAMKRSLAGRYC-----SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGG 108
Db 67 GFLMPVLAGTYRCYGSVPHSPYQ-----LSAPSDPLDIVITGLYEKPSLSAOLGPTVLAGE 122

QY 109 DVTLQCQTRYGFQFPALYKEGDPAFYKNP-----ERWYRASFPITVTAHSGTYRCYSF 163
Db 123 NVTLSCSRSSYDMYHLSREGEAHERRLPAGPKVNGTFAQDFPL--GPATHGGTYRCFGS 180

QY 164 SSRDPYLWSAPSDPLELVVTG 184
Db 181 FHDSPYEWSKSSDPLLVSVTG 201

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RESULT 20

RESUME 20				
Q6QWD6	Q6QWD6	PRELIMINARY;	PRT;	236 AA.
ID	Q6QWD6;			
AC	Q6QWD6;			
DT	05-JUL-2004	(TREMBLrel. 27, Created)		
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE	KIR antigen 3DL1 (Fragment).			
GN	Name=KIR3DL1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Schammel C.M.G., Hurley C.K.;			
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY523804; AAS73160.1; JOINED.			
DR	EMBL; AY523805; AAS73160.1; JOINED.			
DR	EMBL; AY523806; AAS73160.1; -.			
DR	HSSP; P43628; 1B6U.			
DR	InterPro; IPR007110; Ig-like.			
DR	Pfam; PF00047; ig; 2.			
FT	NON_TER 1			
FT	NON_TER 236			
SO	SEQUENCE 236 AA; 25828 MW; 9959A3DD2378CF81 CRC64;			

RESULT 21

RESUBMIT	Q6QWDS	PRELIMINARY;	PRT;	235 AA.
ID	Q6QWDS			
AC	Q6QWDS;			
DT	05-JUL-2004	(TREMBLrel. 27, Created)		
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE	KIR antigen 3DL2 (Fragment).			

GN	Name=KIR3DL2;
OS	Homo sapiens (Human) .
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Schammel C.M.G., Hurley C.K.;
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases .
DR	EMBL; AY523807; AAS73161.1; JOINED.
DR	EMBL; AY523808; AAS73161.1; JOINED.
DR	EMBL; AY523809; AAS73161.1; -.
DR	HSSP; P43628; IB6U.
DR	InterPro; IPR007110; Ig-like.
DR	Pfam; PF00047; ig; 2.
FT	NON_TER 1 1
FT	NON_TER 235 235
SO	SEQUENCE 235 AA; 25771 MW; F56803C029E09258 CRC64;

RESULT 22

ID	Q6QWD4	PRELIMINARY;	PRT;	235 AA.
AC	Q6QWD4;			
DT	05-JUL-2004	(TREMBLrel. 27, Created)		
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TREMBLrel. 27, Last annotation update)		
DE	KIR antigen 3DL2 (Fragment).			
GN	Name=KIR3DL2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Schammel C.M.G., Hurley C.K.;			
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY523810; AAS73162.1; JOINED.			
DR	EMBL; AY523811; AAS73162.1; JOINED.			
DR	EMBL; AY523812; AAS73162.1; -.			
DR	HSSP; P43628; 1B6U.			
DR	InterPro; IPR007110; Ig-like.			
DR	Pfam; PF00047; ig; 2.			
FT	NON_TER 1			
FT	NON_TER 235			
SO	SEQUENCE 235 AA; 25745 MW; 8E0A8100E839AB2D CRC64;			

Db	24	AGTYRC----	RGSRPHSLTGSWSPNSPLVIMVTGNHHRKPSLLAHPGTLLKSGETVILQCWS	80
Qy	117	RYGFDQFALYKEGDPAPYKXNPERWY-----	RASFPITVTAAHSGTYRCYSFSSRDP	168
Db	81	DVMFEHFFLHREGIS----	EDPSRLVGQIHGVSKANFSIGPLMPVLACTYRCYGSVPHSP	137
Qy	169	YLWSAPSDPLELVVTGTSVTPSRRLPTEPPSSVAEFSEATAELTVSFNKNVFTTET-----	223	
Db	138	YQLSAPSDPLDIVITGLYEKPS-LSAQPGPTVQAGENVTLSCSSWSSYDIYHLSREGEAH	196	
Qy	224	SRSITTSPK-----	ESDSPAGPA	241
Db	197	ERRLRAVPKVNRTFQADPFLGPA	219	
RESULT 23				
Q8MI79				
ID	Q8MI79	PRELIMINARY;	PRT;	174 AA.
AC	Q8MI79;			
DT	01-OCT-2002	(TrEMBLrel. 22, Created)		
DT	01-OCT-2002	(TrEMBLrel. 22, Last sequence update)		
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)		
DE	Natural killer cell immunoglobulin-like receptor (Fragment).			
GN	Name=Popy-KIR2DL4;			
OS	Pongo pygmaeus (Orangutan).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.			
OX	NCBI_TaxID=9600;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22072192; PubMed=12077248;			
RA	Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;			
RT	"NK cell receptors of the orangutan (Pongo pygmaeus): a pivotal			
RT	species for tracking the coevolution of killer cell Ig-like receptors			
RT	with MHC-C.;"			
RL	J. Immunol. 169:220-229(2002).			
DR	EMBL; AF470388; AAM78488.1; -.			
DR	HSSP; P43626; INKR.			
DR	GO; GO:0004872; F:receptor activity; IEA.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR007110; Ig-like.			
DR	Pfam; PF00047; ig; 2.			
DR	SMART; SM00409; IG; 1.			
KW	Receptor.			
FT	NON TER 1			
SQ	SEQUENCE 174 AA; 19227 MW; F3C5FDC8FC316C39 CRC64;			
Query Match 18.8%; Score 245; DB 2; Length 174;				
Best Local Similarity 36.5%; Pred. No. 2.1e-11;				
Matches 62; Conservative 27; Mismatches 63; Indels 18; Gaps 5;				
Qy	7	KPSLQALPSSLVPLEKPVTLRCQPPGVDLYRLEKLSS-----	SRYQDQAVLFIPAMK	59
Db	1	KPFCSAWPSAVVPQGGHVTLRCHYRRGFNIFTLYKKDGVVPELYNRFWNSFLISP-VT	59	
Qy	60	RSLAGRYRC---SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQT	116	
Db	60	PAHAGTYRCRGFHPHSPTSEWSAPSNPLVIMVTGLYEKPSLSAQPGPTVCAGENVTLS	119	
Qy	117	RYGFDQFALYKEGDPAPYKXNP-----	ERWYRASFPITVTAAHSGTYRCY	161
Db	120	WSSFDMYHLSREGEAHQLRLPAVPSINGTFQADFPL--	GPATHRGTYRCF	167
RESULT 24				
Q9H7L2				
ID	Q9H7L2	PRELIMINARY;	PRT;	227 AA.
AC	Q9H7L2;			
DT	01-MAR-2001	(TrEMBLrel. 16, Created)		
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE	FLJ00060 protein (Fragment).			
GN	Name=FLJ00060;			

OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RX	PubMed=14702039; DOI=10.1038/ng1285;			
RA	Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,			
RA	Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,			
RA	Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,			
RA	Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,			
RA	Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,			
RA	Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,			
RA	Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,			
RA	Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,			
RA	Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,			
RA	Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,			
RA	Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,			
RA	Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,			
RA	Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,			
RA	Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,			
RA	Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,			
RA	Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,			
RA	Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,			
RA	Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,			
RA	Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,			
RA	Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,			
RA	Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,			
RA	Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,			
RA	Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,			
RA	Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,			
RA	Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,			
RA	Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,			
RA	Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,			
RA	Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;			
RT	"Complete sequencing and characterization of 21,243 full-length human			
RT	cDNAs";			
RL	Nat. Genet. 36:40-45(2004).			
DR	EMBL; AK024467; BAB15757.1; -.			
DR	HSSP; P43627; 2DLI.			
DR	InterPro; IPR007110; Ig-like.			
DR	Pfam; PF00047; ig; 1.			
DR	PROSITE; PS50835; IG-LIKE; 1.			
FT	NON TER 1			
SQ	SEQUENCE 227 AA; 25153 MW; FD0D56B81F5D0F75 CRC64;			
Query Match 18.8%; Score 244.5; DB 2; Length 227;				
Best Local Similarity 31.1%; Pred. No. 3.2e-11;				
Matches 71; Conservative 26; Mismatches 74; Indels 57; Gaps				
QY	2	SGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVD---	LYRLEKLSSRYQDQ-----	
Db	7	SGLFTKPSISAHPPSSLVHAGARVSLRCHSELADEFILYKEGHIQHSQQLDQGM	EAGIHY	
QY	51	--AVLFIPAMKRSLAGRYRC-----SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPG		
Db	67	VEAVFSMGPVTPAHAGAYRC CGCFSHSRYE---WSAPSDPLDIVITGKYKKPSLSTQVD		
QY	102	PAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKXNPERW-----YRASFPITVT		
Db	123	PMMLRLEKLTLCFSSEISFDQYHLFRHG-----VAHGQWLSGGQRHREAFQANFSVGRAT		
QY	152	AAHSGTYRCYSFSSRDPY-----LWSAPSDPLELV 181		
Db	178	PVPGGYRCYGSFNDSPYKPPVTRCNFTPQETLRLVLLCHSQNPPLNLV 225		
RESULT 25				
ID Q99702	PRELIMINARY;		PRT;	151 AA.
AC Q99702;				
DT 01-MAY-1997 (TrEMBLrel. 03, Created)				

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 31, 2005, 17:55:59 ; Search time 163 Seconds
(without alignments)
106.774 Million cell updates/sec

Title: US-09-503-387-3_COPY_44_88
Perfect score: 234
Sequence: 1 VTLRCQPPGVDLYRLEKLS.....DQAVLFIPAMKRSLAGRYRC 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 918587

Minimum DB seq length: 0
Maximum DB seq length: 46

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution..

SUMMARIES

Result No.	Query Match		Length	DB ID	Description
	Score	%			
1	216	92.3	41	4	AAB61258 Human TAN
2	216	92.3	41	6	ABU11224 Human TAN
3	164	70.1	41	4	AAB61271 Mouse TAN
4	164	70.1	41	6	ABU11237 Mouse TAN
5	81	34.6	19	4	AAY72805 Human pla
6	80	34.2	19	4	AAY72798 Human pla
7	69	29.5	19	4	AAY72806 Human pla
8	50	21.4	30	7	ADM35213 Human LY1
9	50	21.4	34	7	ADM34375 Human LY1
10	49	20.9	15	2	AAW78266 Fragment
11	46.5	19.9	45	4	AAG65815 33395 Ig
12	46.5	19.9	45	6	AAE35359 Human pro
13	45.5	19.4	37	3	AAY76375 Fragment
14	45.5	19.4	37	7	ADE12024 Human sec
15	43	18.4	30	7	ADM35214 Human LY1
16	43	18.4	34	7	ADF22079 Bioactive
17	43	18.4	35	7	ADF22052 Bioactive
18	43	18.4	35	7	ADF22020 Bioactive
19	43	18.4	36	7	ADF22925 Bioactive
20	43	18.4	36	7	ADP22957 Bioactive
21	43	18.4	36	7	ADF22893 Bioactive
22	43	18.4	37	7	ADF23053 Bioactive
23	43	18.4	37	7	ADF22989 Bioactive
24	43	18.4	37	7	ADF23021 Bioactive
25	43	18.4	38	7	ADF23117 Bioactive

26	43	18.4	38	7	ADF23085	Adf23085 Bioactive
27	43	18.4	39	7	ADF18773	Adf18773 Bioactive
28	42	17.9	36	7	ADF22973	Adf22973 Bioactive
29	42	17.9	37	7	ADF23069	Adf23069 Bioactive
30	42	17.9	38	7	ADF23133	Adf23133 Bioactive
31	42	17.9	39	7	ADF18789	Adf18789 Bioactive
32	41.5	17.7	41	4	ABB03192	Abb03192 Human mus
33	41.5	17.7	41	6	ABU12486	Abu12486 Novel hum
34	41.5	17.7	41	8	ADJ28512	Adj28512 Human mus
35	41	17.5	20	4	AAy72797	Aay72797 Human pla
36	41	17.5	30	3	AAG06160	Aag06160 Arabidops
37	41	17.5	30	5	AAU85099	Aau85099 Human TRP
38	41	17.5	30	8	ADS33495	Ads33495 cMET-HGF
39	41	17.5	33	7	ADF22690	Adf22690 Bioactive
40	41	17.5	34	7	ADF22083	Adf22083 Bioactive
41	41	17.5	34	7	ADF22177	Adf22177 Bioactive
42	41	17.5	35	7	ADF22024	Adf22024 Bioactive
43	41	17.5	35	7	ADF21988	Adf21988 Bioactive
44	41	17.5	35	7	ADF21926	Adf21926 Bioactive
45	41	17.5	35	7	ADF21866	Adf21866 Bioactive
46	41	17.5	36	7	ADF22929	Adf22929 Bioactive
47	41	17.5	36	7	ADF22941	Adf22941 Bioactive
48	41	17.5	36	7	ADF21914	Adf21914 Bioactive
49	41	17.5	36	7	ADF22897	Adf22897 Bioactive
50	41	17.5	36	7	ADF22961	Adf22961 Bioactive
51	41	17.5	37	7	ADF23057	Adf23057 Bioactive
52	41	17.5	37	7	ADF23025	Adf23025 Bioactive
53	41	17.5	37	7	ADF23037	Adf23037 Bioactive
54	41	17.5	37	7	ADF22993	Adf22993 Bioactive
55	41	17.5	38	7	ADF23089	Adf23089 Bioactive
56	41	17.5	38	7	ADF23121	Adf23121 Bioactive
57	41	17.5	38	7	ADF23101	Adf23101 Bioactive
58	41	17.5	39	7	ADF18777	Adf18777 Bioactive
59	40.5	17.3	43	8	ADK01832	Adk01832 Hepatitis
60	40	17.1	30	8	ADS33636	Ads33636 cMET-HGF
61	40	17.1	34	7	ADF22095	Adf22095 Bioactive
62	40	17.1	35	7	ADF22036	Adf22036 Bioactive
63	40	17.1	36	7	ADF22909	Adf22909 Bioactive
64	40	17.1	36	7	ADF22977	Adf22977 Bioactive
65	40	17.1	37	7	ADF23073	Adf23073 Bioactive
66	40	17.1	37	7	ADF23005	Adf23005 Bioactive
67	40	17.1	38	7	ADF23137	Adf23137 Bioactive
68	40	17.1	39	7	ADF18793	Adf18793 Bioactive
69	39	16.7	25	5	AAE20922	Aae20922 Peptide c
70	39	16.7	30	8	ADS33678	Ads33678 cMET-HGF
71	39	16.7	30	8	ADS33643	Ads33643 cMET-HGF
72	39	16.7	30	8	ADS33756	Ads33756 cMET-HGF
73	39	16.7	32	8	ABO57464	Abo57464 Human gen
74	39	16.7	33	7	ADF22694	Adf22694 Bioactive
75	39	16.7	34	7	ADF22181	Adf22181 Bioactive
76	39	16.7	34	7	ADF22071	Adf22071 Bioactive
77	39	16.7	35	7	ADF22044	Adf22044 Bioactive
78	39	16.7	35	7	ADF21992	Adf21992 Bioactive
79	39	16.7	35	7	ADF22012	Adf22012 Bioactive
80	39	16.7	35	7	ADF21870	Adf21870 Bioactive
81	39	16.7	36	7	ADF22945	Adf22945 Bioactive
82	39	16.7	36	7	ADF21918	Adf21918 Bioactive
83	39	16.7	36	7	ADF22885	Adf22885 Bioactive
84	39	16.7	36	7	ADF22917	Adf22917 Bioactive
85	39	16.7	36	7	ADF22949	Adf22949 Bioactive
86	39	16.7	37	7	ADF23045	Adf23045 Bioactive
87	39	16.7	37	7	ADF22981	Adf22981 Bioactive
88	39	16.7	37	7	ADF23013	Adf23013 Bioactive
89	39	16.7	37	7	ADF23041	Adf23041 Bioactive
90	39	16.7	38	7	ADF23077	Adf23077 Bioactive
91	39	16.7	38	7	ADF23109	Adf23109 Bioactive
92	39	16.7	38	7	ADF23105	Adf23105 Bioactive
93	39	16.7	38	8	ABO54671	Abo54671 Human gen
94	39	16.7	39	7	ADF18765	Adf18765 Bioactive
95	39	16.7	41	3	AAB34631	Aab34631 Gene 2 hu
96	39	16.7	41	3	AAB34632	Aab34632 Human sec
97	39	16.7	42	4	ABB03229	Abb03229 Human mus
98	39	16.7	42	4	AAE13010	Aae13010 Consensus

99 39 16.7 42 6 ABU12523 Abul12523 Novel hum
100 39 16.7 42 8 ADJ28549 Adj28549 Human mus

ALIGNMENTS

RESULT 1
AAB61258
ID AAB61258 standard; protein; 41 AA.
XX AC AAB61258;
XX DT 04-APR-2001 (first entry)
XX DE Human TANGO 268 Ig-like domain #1.
XX KW Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX KW Homo sapiens.
OS OS
XX WO200100810-A1.
XX PN
XX PD 04-JAN-2001.
XX PF 30-JUN-2000; 2000WO-US018152.
XX PR 30-JUN-1999; 99US-00345468.
PR 06-DEC-1999; 99US-00454824.
PR 14-FEB-2000; 2000US-00503387.
XX XX
PA (MILL-) MILLENNIUM PHARM INC.
XX XX
PI Busfield SJ, Villelal J, Jandrot-Perrus M, Vainchencker W;
PI Gill DS, Qian MD, Kingsbury G;
XX XX
DR WPI; 2001-080877/09.
XX XX
PT New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating and
PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological
PT disorders.
XX XX
PS Disclosure; Page 203; 227pp; English.
XX XX
CC The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders (e.g.
CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.
CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
CC immunological diseases (e.g. platelet disorder) and embryonic liver
CC disorders. Preferably they are used to prevent acture cardiac ischaemia
CC following angioplasty and metastatic cancers, especially of the colon and
CC liver
XX XX
SQ Sequence 41 AA;

Query Match' 92.3%; Score 216; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 CQGPFGVDLYRLEKLSRRYQDQAVLFIPAMKRSLAGRYC 45

Db 1 CQGPFGVDLYRLEKLSRRYQDQAVLFIPAMKRSLAGRYC 41

RESULT 2
ABU11224
ID ABU11224 standard; peptide; 41 AA.
XX AC ABU11224;
XX DT 06-FEB-2003 (first entry)
XX DE Human TANGO 268 Ig-like domain #1.
XX KW Human; mouse; variable heavy; VH; antigen; cancer;
KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
KW TANGO 268; extracellular matrix; collagen; platelet release;
KW proliferation; migration; embryogenesis; inflammation; thrombosis;
KW degranulation; thrombocytopaenia; antibody; thrombotic disorder;
KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
KW cardiovascular disease; angina pectoris; myocardial infarction;
KW coronary restenosis; atherosclerosis; immunological disorder;
KW developmental disorder; embryonic disorder; liver disorder;
KW cerebral vascular disease; venous thromboembolism disease.
XX XX
OS Homo sapiens.
XX WO200280968-A1.
XX PN
XX PD 17-OCT-2002.
XX PF 09-APR-2002; 2002WO-US011122.
XX PR 09-APR-2001; 2001US-00829495.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX XX
PI Busfield SJ, Villeval J, Jandrot-Perrus M, Vainchencker W;
PI Gill DS, Qian DM, Kingsbury G;
XX XX
DR WPI; 2003-058477/05.
XX XX
PT Novel substantially purified antibody immunospecifically binding to TANGO
PT 268 antigen, useful for treating bleeding disorders such as
PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.
XX XX
PS Disclosure; Page 212; 236pp; English.
XX XX
CC This invention relates to a novel purified antibody comprising a variable
CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
CC The antibodies of the invention act to decrease or block TANGO 268
CC binding to extracellular matrix components, or as a Collagen or platelet
CC release and aggregating blocker. The antibodies of the invention are
CC useful for modulating proliferation, migration, morphology,
CC differentiation and/or function of megakaryocytes and platelets,
CC including during development e.g. embryogenesis, modulating leukocyte-
CC platelet and platelet-endothelium interactions in inflammation and/or
CC thrombosis, and modulating platelet aggregation and degranulation. They
CC are also useful for modulating disorders associated with abnormal or
CC aberrant megakaryocyte and/or platelet proliferation, migration,
CC morphology, differentiation and/or function, e.g. bleeding disorders such
CC as thrombocytopaenia. Other diseases which may be modulated by these
CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
CC coronary diseases (e.g. cardiovascular diseases including angina
CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
CC etc); immunological disorders, developmental disorders, embryonic
CC disorders, liver disorders, cerebral vascular diseases, venous
CC thromboembolism disease, coronary diseases, and metastatic cancers. The

CC antibodies of the invention only causes a transient decrease in platelet
CC counts, platelet aggregation, and/or platelet activation and so have some
CC advantages over prior art methods. The present sequence represents a
CC peptide sequence used to generate the antibodies of the invention

XX Sequence 41 AA;
SQ Query Match 92.3%; Score 216; DB 6; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 5 CQPPGVLYRLEKLSRRYQDQAVLFIPAMKRSAGRYRC 45
Db 1 CQPPGVLYRLEKLSRRYQDQAVLFIPAMKRSAGRYRC 41

RESULT 3
AAB61271
ID AAB61271 standard; protein; 41 AA.
XX AC AAB61271;
XX DT 04-APR-2001 (first entry)
XX DE Mouse TANGO 268 Ig-like domain #1.
XX KW Mouse; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX Mus musculus.
OS WO200100810-A1.
PN 04-JAN-2001.
PD 30-JUN-2000; 2000WO-US018152.
PF 30-JUN-1999; 99US-00345468.
PR 06-DEC-1999; 99US-00454824.
PR 14-FEB-2000; 2000US-00503387.
XX (MILL-) MILLENNIUM PHARM INC.
XX Busfield SJ, Villelval J, Jandrot-Perrus M, Vainchencker W;
PI Gill DS, Qian MD, Kingsbury G;
XX WPI; 2001-080877/09.
PT New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating and
PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological
PT disorders.
XX Disclosure; Page 210; 227pp; English.

XX The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders (e.g.
CC thrombocytopenia), blood vessel injury, thrombotic disorders (e.g.
CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,
CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),
CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),
CC immunological diseases (e.g. platelet disorder) and embryonic liver
CC disorders. Preferably they are used to prevent acute cardiac ischaemia
CC following angioplasty and metastatic cancers, especially of the colon and

CC liver
XX Sequence 41 AA;
SQ Query Match 70.1%; Score 164; DB 4; Length 41;
Best Local Similarity 73.2%; Pred. No. 4.5e-16;
Matches 30; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
Qy 5 CQPPGVLYRLEKLSRRYQDQAVLFIPAMKRSAGRYRC 45
Db 1 CQPPGVLYRLEKLSRRYQDQAVLFIPAMKRSAGRYRC 41

RESULT 4
ABU11237
ID ABU11237 standard; peptide; 41 AA.
XX AC ABU11237;
XX DT 06-FEB-2003 (first entry)
XX DE Mouse TANGO 268 IgG-like domain.
XX KW Human; mouse; variable heavy; VH; antigen; cancer;
KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
KW TANGO 268; extracellular matrix; collagen; platelet release;
KW proliferation; migration; embryogenesis; inflammation; thrombosis;
KW degranulation; thrombocytopenia; antibody; thrombotic disorder;
KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
KW cardiovascular disease; angina pectoris; myocardial infarction;
KW coronary restenosis; atherosclerosis; immunological disorder;
KW developmental disorder; embryonic disorder; liver disorder;
KW cerebral vascular disease; venous thromboembolism disease.
XX Mus musculus.
OS WO200280968-A1.
PN 17-OCT-2002.
PD 09-APR-2002; 2002WO-US011122.
PF 09-APR-2001; 2001US-00829495.
PR (MILL-) MILLENNIUM PHARM INC.
XX Busfield SJ, Villelval J, Jandrot-Perrus M, Vainchencker W;
PI Gill DS, Qian DM, Kingsbury G;
XX WPI; 2003-058477/05.
PT Novel substantially purified antibody immunospecifically binding to TANGO
PT 268 antigen, useful for treating bleeding disorders such as
PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.
XX Disclosure; Page 219; 236pp; English.

XX This invention relates to a novel purified antibody comprising a variable
CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;
CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically
CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.
CC The antibodies of the invention act to decrease or block TANGO 268
CC binding to extracellular matrix components, or as a Collagen or platelet
CC release and aggregation blocker. The antibodies of the invention are
CC useful for modulating proliferation, migration, morphology,
CC differentiation and/or function of megakaryocytes and platelets,
CC including during development e.g. embryogenesis, modulating leukocyte-
CC platelet and platelet-endothelium interactions in inflammation and/or
CC thrombosis, and modulating platelet aggregation and degranulation. They
CC are also useful for modulating disorders associated with abnormal or
CC aberrant megakaryocyte and/or platelet proliferation, migration,
CC morphology, differentiation and/or function, e.g. bleeding disorders such

CC as thrombocytopaenia. Other diseases which may be modulated by these
CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
CC coronary diseases (e.g. cardiovascular diseases including angina
CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
CC etc); immunological disorders, developmental disorders, embryonic
CC disorders, liver disorders, cerebral vascular diseases, venous
CC thromboembolism disease, coronary diseases, and metastatic cancers. The
CC antibodies of the invention only causes a transient decrease in platelet
CC counts, platelet aggregation, and/or platelet activation and so have some
CC advantages over prior art methods. The present sequence represents a
CC peptide sequence used to generate the antibodies of the invention
XX
SQ Sequence 41 AA;

Query Match 70.1%; Score 164; DB 6; Length 41;
Best Local Similarity 73.2%; Pred. No. 4.5e-16;
Matches 30; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 5 CQPPGVLDLYRLEKLSRRYQDQAVLFIPAMKRSNAGRYRC 45
Db 1 CQPPDVLRYRLEKLEKPEKEDQDFLFIPTMERSNAGRYRC 41

RESULT 5
AAY72805
ID AAY72805 standard; peptide; 19 AA.

XX AAY72805;

DT 31-MAY-2001 (first entry)

XX Human platelet membrane glycoprotein VI (GPVI) peptide 11.

XX Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
KW vascular disease; thrombosis.

XX Homo sapiens.

OS WO200116321-A1.

PN 08-MAR-2001.

XX 01-SEP-2000; 2000WO-US023975.

XX 01-SEP-1999; 99US-0152197P.

PR 08-OCT-1999; 99US-0158251P.

XX (SAKA) OTSUKA PHARM CO LTD.

XX Tandon N, Sun B, Nakamura T, Yamamoto N;

XX WPI; 2001-226691/23.

PT Anti-thrombotic medicament, comprising a polypeptide having the
PT extracellular domain of platelet membrane glycoprotein VI or its variant,
PT useful for treating a vascular disease and reducing platelet activation.

XX Claim 13; Page 58; 74pp; English.

XX The present sequence is a human platelet membrane glycoprotein VI (GPVI)
CC peptide 11. The medicament comprising GPVI is useful for treating
CC vascular disease, and for reducing platelet activation which involves
CC contacting platelets with the medicament. The extracellular portion of
CC GPVI is used therapeutically to attenuate platelet activation and
CC aggregation and to treat thrombosis and other vascular diseases.
CC Antibodies generated against GPVI are used as research and
CC immunotherapeutic agents

XX Sequence 19 AA;

Query Match 34.6%; Score 81; DB 4; Length 19;

Best Local Similarity 89.5%; Pred. No. 0.00023;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 KLSRRYQDQAVLFIPAMK 36
Db 1 KLSRRYQDQAVLFIPMAK 19

RESULT 6
AAY72798
ID AAY72798 standard; peptide; 19 AA.

XX AAY72798;

DT 31-MAY-2001 (first entry)

XX Human platelet membrane glycoprotein VI (GPVI) peptide 5.

XX Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
KW vascular disease; thrombosis.

XX Homo sapiens.

OS Key Location/Qualifiers

FT Misc-difference 4 /label= Unknown

FT Misc-difference 5 /label= Unknown

XX WO200116321-A1.

XX 08-MAR-2001.

XX 01-SEP-2000; 2000WO-US023975.

XX 01-SEP-1999; 99US-0152197P.

PR 08-OCT-1999; 99US-0158251P.

XX (SAKA) OTSUKA PHARM CO LTD.

XX Tandon N, Sun B, Nakamura T, Yamamoto N;

XX WPI; 2001-226691/23.

XX Anti-thrombotic medicament, comprising a polypeptide having the
PT extracellular domain of platelet membrane glycoprotein VI or its variant,
PT useful for treating a vascular disease and reducing platelet activation.

XX Claim 9; Page 58; 74pp; English.

XX The present sequence is a human platelet membrane glycoprotein VI (GPVI)
CC peptide 5. The medicament comprising GPVI is useful for treating vascular
CC disease, and for reducing platelet activation which involves contacting
CC platelets with the medicament. The extracellular portion of GPVI is used
CC therapeutically to attenuate platelet activation and aggregation and to
CC treat thrombosis and other vascular diseases. Antibodies generated
CC against GPVI are used as research and immunotherapeutic agents

XX Sequence 19 AA;

Query Match 34.2%; Score 80; DB 4; Length 19;
Best Local Similarity 84.2%; Pred. No. 0.00032;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 KLSRRYQDQAVLFIPAMK 36
Db 1 KLDXXRYQDQAVLFIPAMK 19

RESULT 7
AAY72806
ID AAY72806 standard; peptide; 19 AA.

XX

AC AAY72806;
XX
DT 31-MAY-2001 (first entry)
XX
DE Human platelet membrane glycoprotein VI (GPVI) peptide 12.
XX
KW Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
KW vascular disease; thrombosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 4 /label= Unknown
FT FT Misc-difference 5 /label= Unknown
FT FT
XX WO200116321-A1.
XX
PD 08-MAR-2001.
XX
PF 01-SEP-2000; 2000WO-US023975.
XX
PR 01-SEP-1999; 99US-0152197P.
PR 08-OCT-1999; 99US-0158251P.
XX
PA (SAKA) OTSUKA PHARM CO LTD.
XX
XX Tandon N, Sun B, Nakamura T, Yamamoto N;
PI WPI; 2001-226691/23.
DR
XX
XX Anti-thrombotic medicament, comprising a polypeptide having the
PT extracellular domain of platelet membrane glycoprotein VI or its variant,
PT useful for treating a vascular disease and reducing platelet activation.
XX
PS Disclosure; Page 17; 74pp; English.
XX
CC The present sequence is a human platelet membrane glycoprotein VI (GPVI)
CC peptide 12. The medicament comprising GPVI is useful for treating
CC vascular disease, and for reducing platelet activation which involves
CC contacting platelets with the medicament. The extracellular portion of
CC GPVI is used therapeutically to attenuate platelet activation and
CC aggregation and to treat thrombosis and other vascular diseases.
CC Antibodies generated against GPVI are used as research and
CC immunotherapeutic agents
XX
SQ Sequence 19 AA;
Query Match 29.5%; Score 69; DB 4; Length 19;
Best Local Similarity 73.7%; Pred. NO. 0.013;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 18 KLSRRYQDQAVLFIPAMK 36
Db 1 KLDXXRYQDQAVLFIPMAK 19
RESULT 8
ADM35213
ID ADM35213 standard; peptide; 30 AA.
XX
AC ADM35213;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human LY1448P cancer related peptide for cancer detection method.
XX
KW cytostatic; T-cell vaccine; detection; cancer;
KW chronic lymphocytic leukemia.
XX
OS Homo sapiens.
XX

PN WO2003077836-A2.
XX
PD 25-SEP-2003.
XX
PF 06-NOV-2002; 2002WO-US035728.
XX
PR 06-NOV-2001; 2001US-00040862.
PR 23-MAY-2002; 2002US-00154884.
XX
PA (CORI-) CORIXA CORP.
XX
XX Gaiger A, Algate PA, Mannion J, Retter M;
PI WPI; 2003-756941/71.
XX
PT Detecting cancer in a patient comprises contacting a biological sample
PT from the patient with a binding agent that binds to a cancer-associated
PT polypeptide and comparing the amount of polypeptide to a predetermined
PT cutoff value.
XX
PS Disclosure; SEQ ID NO 10438; 419pp; English.
XX
CC The invention relates to a method of detecting (M1) cancer in a patient
CC by: (i) contacting a biological sample from the patient with an agent
CC that binds to any of three polypeptides given in the specification; (ii)
CC detecting in a sample an amount of the peptide that binds to the binding
CC agent; and (iii) comparing the amount of polypeptide present in the
CC patient's sample to a predetermined cutoff value. The specification also
CC discloses a separate method for detecting (M2) cancer in a patient by a
CC method similar to M1, except that the detection agent is an
CC oligonucleotide that binds to any of three polynucleotides given in the
CC specification. M1 and M2 are useful for detecting the presence of cancer
CC in a patient, especially chronic lymphocytic leukemia. The applicants
CC have identified specific human polypeptides overexpressed in one or more
CC types of hematological malignancies. This sequence corresponds to a
CC peptide used in the method of the invention.
XX
SQ Sequence 30 AA;
Query Match 21.4%; Score 50; DB 7; Length 30;
Best Local Similarity 61.1%; Pred. No. 13;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 28 AVLFIPAMKRS LAGRYRC 45
Db 11 AELEIPAVKESDAGKYVC 28
RESULT 9
ADM34375
ID ADM34375 standard; peptide; 34 AA.
XX
AC ADM34375;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human LY1448P cancer related peptide for cancer detection method.
XX
KW cytostatic; T-cell vaccine; detection; cancer;
KW chronic lymphocytic leukemia.
XX
OS Homo sapiens.
XX
PN WO2003077836-A2.
XX
PD 25-SEP-2003.
XX
PF 06-NOV-2002; 2002WO-US035728.
XX
PR 06-NOV-2001; 2001US-00040862.
PR 23-MAY-2002; 2002US-00154884.
XX
PA (CORI-) CORIXA CORP.
XX


```

KW antiarthritic; neuroprotective; dermatological; immunosuppressive;
KW antiinflammatory; antiasthmatic; antiulcer; antianaemic; hepatotropic.
XX
XX Homo sapiens.
XX WO200172827-A2.
XX
XX 04-OCT-2001.
XX
XX 23-MAR-2001; 2001WO-US009470.
XX
XX 24-MAR-2000; 2000US-0191863P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Glucksmann MA;
XX
XX WPI; 2001-626254/72.
XX
XX New polypeptide for preventing or treating disorders associated with
XX cellular adhesion, proliferation or differentiation, comprises
XX polypeptide 33395, a member of the leucine rich repeat protein family.
XX
XX Disclosure; Fig 4A-B; 133pp; English.
XX
XX The invention provides an isolated nucleic acid encoding a polypeptide of
XX the leucine rich repeat (LRR) family, designated 33395. The 33395
XX polypeptide can be expressed by standard recombinant methodology. The
XX 33395 polynucleotides and polypeptide can be used to prevent or treat
XX disorders associated with 33395 expression, for example those involving
XX aberrant cellular adhesion, proliferation or differentiation. Specific
XX examples include meloblastoma, juvenile AIDS, diabetes mellitus,
XX rheumatoid arthritis, systemic lupus erythematosus, multiple sclerosis,
XX Chron's disease, ulcerative colitis, asthma, anemia, and chronic active
XX hepatitis. Sequences AAG65815-817 represent consensus amino acid
XX sequences derived from a hidden Markov model corresponding to the
XX immunoglobulin domains of the the human 33395 polypeptide
XX
XX Sequence 45 AA;
XX
XX Query Match 19.9%; Score 46.5; DB 4; Length 45;
XX Best Local Similarity 34.7%; Pred. No. 67;
XX Matches 17; Conservative 0; Mismatches 19; Indels 13; Gaps 2;
XX
XX QY 1 VTLRCQ---GPPGVLDLYRLKLSRRYQDQAVLFIPAMKRSLAGRYRC 45
XX ||||| ||||| ||||| ||||| ||||| |||||
XX Db 4 VTLTCSVSGFGPPPTVTLNRNGKLS-----LTISVTPEDSGGTYTC 43
XX
XX RESULT 12
XX AAE35359
XX ID AAE35359 standard; protein; 45 AA.
XX
XX AC AAE35359;
XX
XX DT 17-JUN-2003 (first entry)
XX
XX XX Human protein related to the invention.
XX
XX DE Human; sodium channel beta-4 subunit; 98359 protein; gene therapy; AIDS;
XX shock; hypertension; psychiatric disease; obsessive-compulsive disorder;
XX bipolar affective disorder; attention deficit disorder; phobic disorder;
XX cardiovascular disorder; neurological disorder; spinocerebellar ataxia;
XX Alzheimer's disease; Parkinson's disease; Tourette's syndrome; anxiety;
XX autoimmune disorder; cellular proliferative disorder; Krabbe's disease;
XX metabolic disorder; multiple sclerosis; cardiomyopathy; liver disorder;
XX bone metabolism disorder; endothelial cell disorder; viral encephalitis;
XX acquired immune deficiency syndrome; peripheral neuropathy; arrhythmia;
XX poliomyelitis; demyelinating disease; leukodystrophy; epilepsy; cancer;
XX dementia; Leigh disease; heart failure; diabetes; arthritis; rabies;
XX pain.
XX
XX OS Homo sapiens.

```


		Matches	13;	Conservative	2;	Mismatches	13;	Indels	11;	Gaps	1;
QY		7	GPPGV	DLRL	LEKLS	SRYYQ	QAVL	FIPAM	KRSL	AGRYRC	45
								:			
Db		1	GPP	-----	SPRGL	PSLP	LHL	PAP	RRYL	QSR	28
RESULT 15											
ADM35214											
ID		ADM35214		standard;		peptide;		30	AA.		
XX		AC		ADM35214;							
XX		DT		03-JUN-2004		(first entry)					
XX		DE		Human LY1448P		cancer related peptide for cancer detection method.					
XX		KW		cytostatic;		T-cell vaccine;		detection;		cancer;	
KW		KW		chronic lymphocytic leukemia.							
XX		OS		Homo sapiens.							
XX		PN		WO2003077836-A2.							
XX		PD		25-SEP-2003.							
XX		PF		06-NOV-2002;		2002WO-US035728.					
XX		PR		06-NOV-2001;		2001US-00040862.					
PR		23-MAY-2002;		2002US-00154884.							
XX		PA		(CORI-) CORIXA CORP.							
XX		PI		Gaiger A, Algate PA, Mannion J, Retter M;							
XX		DR		WPI; 2003-756941/71.							
XX		PT		Detecting cancer in a patient comprises contacting a biological sample							
PT		from the patient with a binding agent that binds to a cancer-associated									
PT		polypeptide and comparing the amount of polypeptide to a predetermined									
PT		cutoff value.									
XX		PS		Disclosure; SEQ ID NO 10439; 419pp; English.							
XX		CC		The invention relates to a method of detecting (M1) cancer in a patient							
CC		by: (i) contacting a biological sample from the patient with an agent									
CC		that binds to any of three polypeptides given in the specification; (ii)									
CC		detecting in a sample an amount of the peptide that binds to the binding									
CC		agent; and (iii) comparing the amount of polypeptide present in the									
CC		patient's sample to a predetermined cutoff value. The specification also									
CC		discloses a separate method for detecting (M2) cancer in a patient by a									
CC		method similar to M1, except that the detection agent is an									
CC		oligonucleotide that binds to any of three polynucleotides given in the									
CC		specification. M1 and M2 are useful for detecting the presence of cancer									
CC		in a patient, especially chronic lymphocytic leukemia. The applicants									
CC		have identified specific human polypeptides overexpressed in one or more									
CC		types of hematological malignancies. This sequence corresponds to a									
CC		peptide used in the method of the invention.									
XX		Sequence 30 AA;									
SQ											
Query Match 18.4%; Score 43; DB 7; Length 30;											
Best Local Similarity 61.5%; Pred. No. 1.3e+02;											
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;											
QY		33	PAMKR	SLAGRYRC		45					
Db		1	PAVKES	DAGKYC		13					
RESULT 16											
ADF22079											
ID		ADF22079		standard;		peptide;		34	AA.		

XX		ADF22079;									
AC		12-FEB-2004		(first entry)							
DT		Bioactive keratin peptide (SeqID 5734).									
XX		keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;									
XX		antiinflammatory; antiulcer; vulnerary; analgesic;									
KW		cell proliferation activator; deodourant; cleanser; toenail care;									
KW		sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.									
XX		Unidentified.									
OS		WO2003064449-A2.									
XX		07-AUG-2003.									
XX		28-JAN-2003; 2003WO-US002645.									
PF		28-JAN-2002; 2002US-0352396P.									
XX		(KERA-) KERAPLAST TECHNOLOGIES INC.									
XX		Cowsar DR;									
PI		WPI; 2003-812322/76.									
DR		Composition comprising an isolated bioactive keratin peptides useful for									
XX		cosmetic preparation, and treating conditions involving damaged, aged and									
PT		diseased epithelial tissue and skin.									
PT		Disclosure; SEQ ID NO 5734; 158pp; English.									
XX		This invention relates to a novel composition comprising an isolated									
CC		bioactive keratin peptide of 4-39 amino acids in length. Specifically, it									
CC		refers to keratin proteins that can stimulate the growth of dermal									
CC		fibroblasts for use in treating damaged, aged or diseased epithelial									
CC		tissue and skin. Furthermore, they exhibit cytokine-like activity,									
CC		particularly cell differentiation, adhesion and migration, and in									
CC		combination with other growth factors can be used to enhance the healing									
CC		activity of damaged skin or bone tissue. The present invention describes									
CC		these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and									
CC		cell proliferation activators. Accordingly, there are various									
CC		applications for cosmetics e.g. deodourant, cleanser and toenail care									
CC		compositions, also in topical applications to damaged epithelial tissue									
CC		from sunburn, ulcers or puncture wounds so as to relieve pain, burning or									
CC		itching. The compositions can further be used to treat Crohn's disease,									
CC		skin grafts or diabetic ulcers. This peptide sequence, derived from human									
CC		hair or sheep wool keratin proteins, is a biologically active keratin									
CC		peptide of the invention.									
XX		Sequence 34 AA;									
SQ											
Query Match 18.4%; Score 43; DB 7; Length 34;											
Best Local Similarity 35.3%; Pred. No. 1.6e+02;											
Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;											
QY		2	TLRCQ	-----	-----	GPPGV	DLRL	LEKLS	SRYYQ	25	
Db		1	TLRCQ	GLDRL	NVEVD	AAPT	VDL	NRV	LN	ETRSQYE	34
RESULT 17											
ADF22052											
ID		ADF22052		standard;		peptide;		35	AA.		
XX		AC		ADF22052;							
XX		DT		12-FEB-2004		(first entry)					
XX		DE		Bioactive keratin peptide (SeqID 5927).							

KW keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;
KW antiinflammatory; antiulcer; vulnery; analgesic;
KW cell proliferation activator; deodourant; cleanser; toenail care;
KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.
XX
OS Unidentified.
XX
PN WO2003064449-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-US002645.
XX
PR 28-JAN-2002; 2002US-0352396P.
XX
PA (KERA-) KERAPLAST TECHNOLOGIES INC.
XX
PI Cowsar DR;
XX
DR WPI; 2003-812322/76.
XX
XX Composition comprising an isolated bioactive keratin peptides useful for
PT cosmetic preparation, and treating conditions involving damaged, aged and
PT diseased epithelial tissue and skin.
XX
PS Disclosure; SEQ ID NO 5927; 158pp; English.
XX
CC This invention relates to a novel composition comprising an isolated
CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it
CC refers to keratin proteins that can stimulate the growth of dermal
CC fibroblasts for use in treating damaged, aged or diseased epithelial
CC tissue and skin. Furthermore, they exhibit cytokine-like activity,
CC particularly cell differentiation, adhesion and migration, and in
CC combination with other growth factors can be used to enhance the healing
CC activity of damaged skin or bone tissue. The present invention describes
CC these peptides as antiinflammatory, antiulcer, vulnery, analgesic and
CC cell proliferation activators. Accordingly, there are various
CC applications for cosmetics e.g. deodourant, cleanser and toenail care
CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or
CC itching. The compositions can further be used to treat Crohn's disease,
CC skin grafts or diabetic ulcers. This peptide sequence, derived from human
CC hair or sheep wool keratin proteins, is a biologically active keratin
CC peptide of the invention.
XX
SQ Sequence 35 AA;

Query Match 18.4%; Score 43; DB 7; Length 35;
Best Local Similarity 35.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

QY 2 TLRCQ-----GPPGVDLYRLEKLSRRYQ 25
| | | | | : | | | : | : | :
DB 1 TLRCQLGDRNLNVEVDAAPTVDLNRVLNETRSQYE 34

RESULT 18
ADF22020
ID ADF22020 standard; peptide; 35 AA.
XX
AC ADF22020;
XX
DT 12-FEB-2004 (first entry)
XX
DE Bioactive keratin peptide (SeqID 5895).
XX
KW keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;
KW antiinflammatory; antiulcer; vulnery; analgesic;
KW cell proliferation activator; deodourant; cleanser; toenail care;
KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.
XX
OS Unidentified.
XX

PN WO2003064449-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-US002645.
XX
PR 28-JAN-2002; 2002US-0352396P.
XX
PA (KERA-) KERAPLAST TECHNOLOGIES INC.
XX
PI Cowsar DR;
XX
DR WPI; 2003-812322/76.
XX
XX Composition comprising an isolated bioactive keratin peptides useful for
PT cosmetic preparation, and treating conditions involving damaged, aged and
PT diseased epithelial tissue and skin.
XX
PS Disclosure; SEQ ID NO 5895; 158pp; English.
XX
CC This invention relates to a novel composition comprising an isolated
CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it
CC refers to keratin proteins that can stimulate the growth of dermal
CC fibroblasts for use in treating damaged, aged or diseased epithelial
CC tissue and skin. Furthermore, they exhibit cytokine-like activity,
CC particularly cell differentiation, adhesion and migration, and in
CC combination with other growth factors can be used to enhance the healing
CC activity of damaged skin or bone tissue. The present invention describes
CC these peptides as antiinflammatory, antiulcer, vulnery, analgesic and
CC cell proliferation activators. Accordingly, there are various
CC applications for cosmetics e.g. deodourant, cleanser and toenail care
CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or
CC itching. The compositions can further be used to treat Crohn's disease,
CC skin grafts or diabetic ulcers. This peptide sequence, derived from human
CC hair or sheep wool keratin proteins, is a biologically active keratin
CC peptide of the invention.
XX
SQ Sequence 35 AA;

Query Match 18.4%; Score 43; DB 7; Length 35;
Best Local Similarity 35.3%; Pred. No. 1.6e+02;
Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

QY 2 TLRCQ-----GPPGVDLYRLEKLSRRYQ 25
| | | | | : | | | : | : | :
DB 2 TLRCQLGDRNLNVEVDAAPTVDLNRVLNETRSQYE 35

RESULT 19
ADF22925
ID ADF22925 standard; peptide; 36 AA.
XX
AC ADF22925;
XX
DT 12-FEB-2004 (first entry)
XX
DE Bioactive keratin peptide (SeqID 6055).
XX
KW keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;
KW antiinflammatory; antiulcer; vulnery; analgesic;
KW cell proliferation activator; deodourant; cleanser; toenail care;
KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.
XX
OS Unidentified.
XX
PN WO2003064449-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-US002645.
XX
PR 28-JAN-2002; 2002US-0352396P.
XX

XX (KERA-) KERAPLAST TECHNOLOGIES INC.
XX Cowsar DR;
XX WPI; 2003-812322/76.
XX
XX Composition comprising an isolated bioactive keratin peptides useful for
XX cosmetic preparation, and treating conditions involving damaged, aged and
XX diseased epithelial tissue and skin.
XX
XX Disclosure; SEQ ID NO 6055; 158pp; English.
XX
XX This invention relates to a novel composition comprising an isolated
XX bioactive keratin peptide of 4-39 amino acids in length. Specifically, it
XX refers to keratin proteins that can stimulate the growth of dermal
XX fibroblasts for use in treating damaged, aged or diseased epithelial
XX tissue and skin. Furthermore, they exhibit cytokine-like activity,
XX particularly cell differentiation, adhesion and migration, and in
XX combination with other growth factors can be used to enhance the healing
XX activity of damaged skin or bone tissue. The present invention describes
XX these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and
XX cell proliferation activators. Accordingly, there are various
XX applications for cosmetics e.g. deodorant, cleanser and toenail care
XX compositions, also in topical applications to damaged epithelial tissue
XX from sunburn, ulcers or puncture wounds so as to relieve pain, burning or
XX itching. The compositions can further be used to treat Crohn's disease,
XX skin grafts or diabetic ulcers. This peptide sequence, derived from human
XX hair or sheep wool keratin proteins, is a biologically active keratin
XX peptide of the invention.
XX
SQ Sequence 36 AA;
Query Match 18.4%; Score 43; DB 7; Length 36;
Best Local Similarity 35.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;
QY 2 TLRCQ-----GPPGVLDYRLEKLSRRYQ 25
Db 2 TLRCQLGRLNVEVDAAPTVDLNRVLNETRSQYE 35
RESULT 20
ADF22957
ID ADF22957 standard; peptide; 36 AA.
XX
XX ADF22957;
AC
XX 12-FEB-2004 (first entry)
DT
XX
XX Bioactive keratin peptide (SeqID 6087).
DE
XX
XX keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;
KW antiinflammatory; antiulcer; vulnerary; analgesic;
KW cell proliferation activator; deodorant; cleanser; toenail care;
KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.
XX
XX Unidentified.
OS
XX
XX WO2003064449-A2.
PN
XX
XX 07-AUG-2003.
PD
XX
XX 28-JAN-2003; 2003WO-US002645.
PF
XX
XX 28-JAN-2002; 2002US-0352396P.
PR
XX
XX (KERA-) KERAPLAST TECHNOLOGIES INC.
PA
XX
XX Cowsar DR;
PI
XX
XX WPI; 2003-812322/76.
DR
XX

PT Composition comprising an isolated bioactive keratin peptides useful for
PT cosmetic preparation, and treating conditions involving damaged, aged and
XX diseased epithelial tissue and skin.
XX
XX Disclosure; SEQ ID NO 6087; 158pp; English.
XX
XX This invention relates to a novel composition comprising an isolated
XX bioactive keratin peptide of 4-39 amino acids in length. Specifically, it
XX refers to keratin proteins that can stimulate the growth of dermal
XX fibroblasts for use in treating damaged, aged or diseased epithelial
XX tissue and skin. Furthermore, they exhibit cytokine-like activity,
XX particularly cell differentiation, adhesion and migration, and in
XX combination with other growth factors can be used to enhance the healing
XX activity of damaged skin or bone tissue. The present invention describes
XX these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and
XX cell proliferation activators. Accordingly, there are various
XX applications for cosmetics e.g. deodorant, cleanser and toenail care
XX compositions, also in topical applications to damaged epithelial tissue
XX from sunburn, ulcers or puncture wounds so as to relieve pain, burning or
XX itching. The compositions can further be used to treat Crohn's disease,
XX skin grafts or diabetic ulcers. This peptide sequence, derived from human
XX hair or sheep wool keratin proteins, is a biologically active keratin
XX peptide of the invention.
XX
SQ Sequence 36 AA;
Query Match 18.4%; Score 43; DB 7; Length 36;
Best Local Similarity 35.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;
QY 2 TLRCQ-----GPPGVLDYRLEKLSRRYQ 25
Db 1 TLRCQLGRLNVEVDAAPTVDLNRVLNETRSQYE 34
RESULT 21
ADF22893
ID ADF22893 standard; peptide; 36 AA.
XX
XX ADF22893;
AC
XX
XX 12-FEB-2004 (first entry)
DT
XX
XX Bioactive keratin peptide (SeqID 6023).
DE
XX
XX keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;
KW antiinflammatory; antiulcer; vulnerary; analgesic;
KW cell proliferation activator; deodorant; cleanser; toenail care;
KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.
XX
XX Unidentified.
OS
XX
XX WO2003064449-A2.
PN
XX
XX 07-AUG-2003.
PD
XX
XX 28-JAN-2003; 2003WO-US002645.
PF
XX
XX 28-JAN-2002; 2002US-0352396P.
PR
XX
XX (KERA-) KERAPLAST TECHNOLOGIES INC.
PA
XX
XX Cowsar DR;
PI
XX
XX WPI; 2003-812322/76.
DR
XX
XX Composition comprising an isolated bioactive keratin peptides useful for
XX cosmetic preparation, and treating conditions involving damaged, aged and
XX diseased epithelial tissue and skin.
XX
XX Disclosure; SEQ ID NO 6023; 158pp; English.
XX
XX This invention relates to a novel composition comprising an isolated

CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it
CC refers to keratin proteins that can stimulate the growth of dermal
CC fibroblasts for use in treating damaged, aged or diseased epithelial
CC tissue and skin. Furthermore, they exhibit cytokine-like activity,
CC particularly cell differentiation, adhesion and migration, and in
CC combination with other growth factors can be used to enhance the healing
CC activity of damaged skin or bone tissue. The present invention describes
CC these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and
CC cell proliferation activators. Accordingly, there are various
CC applications for cosmetics e.g. deodourant, cleanser and toenail care
CC compositions, also in topical applications to damaged epithelial tissue
CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or
CC itching. The compositions can further be used to treat Crohn's disease,
CC skin grafts or diabetic ulcers. This peptide sequence, derived from human
CC hair or sheep wool keratin proteins, is a biologically active keratin
CC peptide of the invention.

XX SQ Sequence 36 AA;

Query Match 18.4%; Score 43; DB 7; Length 36;
Best Local Similarity 35.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

QY 2 TLRCQ-----GPPGVDLYRLEKLSRRYQ 25
||||| :||| : :|||
Db 3 TLRCQLGDRLNVEVDAAPTVDLNRVLNETRSQYE 36

RESULT 22

ADDF23053
ID ADF23053 standard; peptide; 37 AA.

XX AC ADF23053;

XX DT 12-FEB-2004 (first entry)

XX DE Bioactive keratin peptide (SeqID 6183).

XX KW keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;
KW antiinflammatory; antiulcer; vulnerary; analgesic;
KW cell proliferation activator; deodourant; cleanser; toenail care;
KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.

XX OS Unidentified.

XX PN WO2003064449-A2.

XX PD 07-AUG-2003.

XX PF 28-JAN-2003; 2003WO-US002645.

XX PR 28-JAN-2002; 2002US-0352396P.

XX PA (KERA-) KERAPLAST TECHNOLOGIES INC.

XX PI Cowsar DR;

XX PS WPI; 2003-812322/76.

XX CC Composition comprising an isolated bioactive keratin peptides useful for
PT cosmetic preparation, and treating conditions involving damaged, aged and
PT diseased epithelial tissue and skin.

XX PS Disclosure; SEQ ID NO 6183; 158pp; English.

XX CC This invention relates to a novel composition comprising an isolated
CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it
CC refers to keratin proteins that can stimulate the growth of dermal
CC fibroblasts for use in treating damaged, aged or diseased epithelial
CC tissue and skin. Furthermore, they exhibit cytokine-like activity,
CC particularly cell differentiation, adhesion and migration, and in
CC combination with other growth factors can be used to enhance the healing
CC activity of damaged skin or bone tissue. The present invention describes

CC these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and
CC cell proliferation activators. Accordingly, there are various
CC applications for cosmetics e.g. deodourant, cleanser and toenail care
CC compositions, also in topical applications to damaged epithelial tissue
CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or
CC itching. The compositions can further be used to treat Crohn's disease,
CC skin grafts or diabetic ulcers. This peptide sequence, derived from human
CC hair or sheep wool keratin proteins, is a biologically active keratin
CC peptide of the invention.

XX SQ Sequence 37 AA;

Query Match 18.4%; Score 43; DB 7; Length 37;
Best Local Similarity 35.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

QY 2 TLRCQ-----GPPGVDLYRLEKLSRRYQ 25
||||| :||| : :|||
Db 2 TLRCQLGDRLNVEVDAAPTVDLNRVLNETRSQYE 35

RESULT 23

ADDF22989
ID ADF22989 standard; peptide; 37 AA.

XX AC ADF22989;

XX DT 12-FEB-2004 (first entry)

XX DE Bioactive keratin peptide (SeqID 6119).

XX KW keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;
KW antiinflammatory; antiulcer; vulnerary; analgesic;
KW cell proliferation activator; deodourant; cleanser; toenail care;
KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.

XX OS Unidentified.

XX PN WO2003064449-A2.

XX PD 07-AUG-2003.

XX PF 28-JAN-2003; 2003WO-US002645.

XX PR 28-JAN-2002; 2002US-0352396P.

XX PA (KERA-) KERAPLAST TECHNOLOGIES INC.

XX PI Cowsar DR;

XX PS WPI; 2003-812322/76.

XX CC Composition comprising an isolated bioactive keratin peptides useful for
PT cosmetic preparation, and treating conditions involving damaged, aged and
PT diseased epithelial tissue and skin.

XX PS Disclosure; SEQ ID NO 6119; 158pp; English.

XX CC This invention relates to a novel composition comprising an isolated
CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it
CC refers to keratin proteins that can stimulate the growth of dermal
CC fibroblasts for use in treating damaged, aged or diseased epithelial
CC tissue and skin. Furthermore, they exhibit cytokine-like activity,
CC particularly cell differentiation, adhesion and migration, and in
CC combination with other growth factors can be used to enhance the healing
CC activity of damaged skin or bone tissue. The present invention describes

XX CC these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and
CC cell proliferation activators. Accordingly, there are various
CC applications for cosmetics e.g. deodourant, cleanser and toenail care
CC compositions, also in topical applications to damaged epithelial tissue
CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or
CC itching. The compositions can further be used to treat Crohn's disease,
CC skin grafts or diabetic ulcers. This peptide sequence, derived from human

CC hair or sheep wool keratin proteins, is a biologically active keratin
CC peptide of the invention.

XX
SQ Sequence 37 AA;

Query Match 18.4%; Score 43; DB 7; Length 37;
Best Local Similarity 35.3%; Pred. No. 1.7e+02;
Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;

QY 2 TLRCQ-----GPPGVDLRLEKLSRRYQ 25
||||| : : : : :
Db 4 TLRCQLGDRNLNVEVDAAPTVDLNRVLNETRSQYE 37

RESULT 24
ADF23021
ID ADF23021 standard; peptide; 37 AA.

XX ADF23021;
AC
XX
XX
DT 12-FEB-2004 (first entry)
XX
DE Bioactive keratin peptide (SeqID 6151).
XX
KW keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;
KW antiinflammatory; antiulcer; vulnerary; analgesic;
KW cell proliferation activator; deodourant; cleanser; toenail care;
KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.

XX
OS Unidentified.

XX
PN WO2003064449-A2.

XX
PD 07-AUG-2003.

XX
PF 28-JAN-2003; 2003WO-US002645.

XX
PR 28-JAN-2002; 2002US-0352396P.

XX
PA (KERA-) KERAPLAST TECHNOLOGIES INC.

XX
PI Cowsar DR;

XX
DR WPI; 2003-812322/76.

XX
XX Composition comprising an isolated bioactive keratin peptides useful for
PT cosmetic preparation, and treating conditions involving damaged, aged and
PT diseased epithelial tissue and skin.

PS Disclosure; SEQ ID NO 6151; 158pp; English.

XX
XX This invention relates to a novel composition comprising an isolated
CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it
CC refers to keratin proteins that can stimulate the growth of dermal
CC fibroblasts for use in treating damaged, aged or diseased epithelial
CC tissue and skin. Furthermore, they exhibit cytokine-like activity,
CC particularly cell differentiation, adhesion and migration, and in
CC combination with other growth factors can be used to enhance the healing
CC activity of damaged skin or bone tissue. The present invention describes
CC these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and
CC cell proliferation activators. Accordingly, there are various
CC applications for cosmetics e.g. deodourant, cleanser and toenail care
CC compositions, also in topical applications to damaged epithelial tissue
CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or
CC itching. The compositions can further be used to treat Crohn's disease,
CC skin grafts or diabetic ulcers. This peptide sequence, derived from human
CC hair or sheep wool keratin proteins, is a biologically active keratin
CC peptide of the invention.

XX
SQ Sequence 37 AA;

Query Match 18.4%; Score 43; DB 7; Length 37;
Best Local Similarity 35.3%; Pred. No. 1.7e+02;

Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;
QY 2 TLRCQ-----GPPGVDLRLEKLSRRYQ 25
||||| : : : : :
Db 3 TLRCQLGDRNLNVEVDAAPTVDLNRVLNETRSQYE 36

RESULT 25
ADF23117
ID ADF23117 standard; peptide; 38 AA.

XX
AC ADF23117;

XX
DT 12-FEB-2004 (first entry)

XX
DE Bioactive keratin peptide (SeqID 6247).

XX
KW keratin; dermal fibroblast; epithelial tissue; cytokine-like activity;
KW antiinflammatory; antiulcer; vulnerary; analgesic;
KW cell proliferation activator; deodourant; cleanser; toenail care;
KW sunburn; puncture wound; Crohn's disease; skin graft; diabetic ulcer.

XX
OS Unidentified.

XX
PN WO2003064449-A2.

XX
PD 07-AUG-2003.

XX
PF 28-JAN-2003; 2003WO-US002645.

XX
PR 28-JAN-2002; 2002US-0352396P.

XX
PA (KERA-) KERAPLAST TECHNOLOGIES INC.

XX
PI Cowsar DR;

XX
DR WPI; 2003-812322/76.

XX
XX Composition comprising an isolated bioactive keratin peptides useful for
PT cosmetic preparation, and treating conditions involving damaged, aged and
PT diseased epithelial tissue and skin.

PS Disclosure; SEQ ID NO 6247; 158pp; English.

XX
XX This invention relates to a novel composition comprising an isolated
CC bioactive keratin peptide of 4-39 amino acids in length. Specifically, it
CC refers to keratin proteins that can stimulate the growth of dermal
CC fibroblasts for use in treating damaged, aged or diseased epithelial
CC tissue and skin. Furthermore, they exhibit cytokine-like activity,
CC particularly cell differentiation, adhesion and migration, and in
CC combination with other growth factors can be used to enhance the healing
CC activity of damaged skin or bone tissue. The present invention describes
CC these peptides as antiinflammatory, antiulcer, vulnerary, analgesic and
CC cell proliferation activators. Accordingly, there are various
CC applications for cosmetics e.g. deodourant, cleanser and toenail care
CC compositions, also in topical applications to damaged epithelial tissue
CC from sunburn, ulcers or puncture wounds so as to relieve pain, burning or
CC itching. The compositions can further be used to treat Crohn's disease,
CC skin grafts or diabetic ulcers. This peptide sequence, derived from human
CC hair or sheep wool keratin proteins, is a biologically active keratin
CC peptide of the invention.

XX
SQ Sequence 38 AA;

Query Match 18.4%; Score 43; DB 7; Length 38;
Best Local Similarity 35.3%; Pred. No. 1.8e+02;

Matches 12; Conservative 4; Mismatches 8; Indels 10; Gaps 1;
QY 2 TLRCQ-----GPPGVDLRLEKLSRRYQ 25
||||| : : : : :
Db 3 TLRCQLGDRNLNVEVDAAPTVDLNRVLNETRSQYE 36

Search completed: October 31, 2005, 17:58:53
Job time : 166 secs

COMPUTER READABLE FORM:
MEDIUM TYPE: 3 5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,385
FILING DATE: No. 6017692ember 8, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Karen F. Lech
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/252001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-554-385-23

Query Match	16.7%;	Score 39;	DB 3;	Length 36;
Best Local Similarity	52.6%;	Pred. No. 1e+02;		
Matches 10;	Conservative	3;	Mismatches	4;
			Indels	2;
			Gaps	1;

Qy 3 LRCQPPGVDLYRLEKLSS 21
||| ||| : ||| : : |||
Db 10 LRLVGTPGAEL--LKKISS 26

RESULT 6
US-08-429-764A-3
; Sequence 3, Application US/08429764A
; Patent No. 5830647
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: de Sauvage, Frederic J.
; TITLE OF INVENTION: MPL LICAND
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,764A
; FILING DATE: 26-Apr-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/348658
; FILING DATE: 02-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185607
; FILING DATE: 21-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/176553
; FILING DATE: 03-JAN-1994
; ATTORNEY/AGENT INFORMATION:

NAME: Winter, Daryl B.
REGISTRATION NUMBER: 32,637
REFERENCE/DOCKET NUMBER: P0871P1C1D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1249
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-429-764A-3

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Query Match      16.2%; Score 38; DB 2; Length 42;
Best Local Similarity 47.4%; Pred. No. 1.8e+02;
Matches 9; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
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QY 1 VTLRCQGPFGVDLYRLEKL 19
: || || || || ||
Db 13 LTLSSPAPPACDLRVLSKL 31

RESULT 7
US-09-461-697-393
; Sequence 393, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 1001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 393
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-697-393

Query Match 16.0%; Score 37.5; DB 3; Length 35;
Best Local Similarity 47.4%; Pred. No. 1.7e+02;
Matches 9; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

Qy 26 DQAV-LFIPAMKRSLAGRY 43
||| :|| :|| :||
Db 14 DQAGVFCPVLFRSRSGHY 32

RESULT 8
US-07-662-007B-30
; Sequence 30, Application US/07662007B
; Patent No. 5344771
; GENERAL INFORMATION:
; APPLICANT: Davies, Huw Maelor
; APPLICANT: Pollard, Michael Roman
; APPLICANT: Voekler, Toni Alois
; APPLICANT: Thompson, Gregory A.
; TITLE OF INVENTION: Plant Thioesterases
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis

```

; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: MicrosoftWord 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/662,007B
; FILING DATE: 19910408
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/514,030
; FILING DATE: 26-APR-1990
; APPLICATION NUMBER: 07/620,426
; FILING DATE: 30-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: CGNE 70-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 916-753-6313
; TELEFAX: 916-753-1510
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-662-007B-30

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Query Match 15.6%; Score 36.5; DB 1; Length 23;
Best Local Similarity 36.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

Qy	12	DLYRLEKLSRRYQDQAVLFIP	33
		: :	
Dd	3	DTRRLQKVNDD-VEDEYLVFIP	23

RESULT 9
US-07-824-247-30
; Sequence 30, Application US/07824247
; Patent No. 5512482
; GENERAL INFORMATION:
; APPLICANT: Voelker, Toni Alois
; TITLE OF INVENTION: Plant Thioesterases
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 720 KB storage
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.7
; SOFTWARE: MicrosoftWord 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/824,247
; FILING DATE: 19920122
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/782,263
; FILING DATE: 24-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/773,096
; FILING DATE: 7-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/704,861
;

```

; FILING DATE: 21-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02960
; FILING DATE: 25-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/562,007
; FILING DATE: 27-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/620,426
; FILING DATE: 30-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/514,030
; FILING DATE: 26-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth Lassen
; REGISTRATION NUMBER: 31,845
; NAME: Donna E. Scherer
; REGISTRATION NUMBER: 34,719
; REFERENCE/DOCKET NUMBER: CGNE 82-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 916-753-6313
; TELEFAX: 916-753-1510
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-07-824-247-30

```

Query Match	15.6%	Score	36.5;	DB	1;	Length	23;
Best Local Similarity	36.4%;	Pred. NO.	1.4e+02;				
Matches	8;	Conservative	7;	Mismatches	6;	Indels	1;
						Gaps	1;

Qy	12	DLYRLEKLS	SSRYQDQ	AVLFIP	33
	:	:	:	:	:
	:	:	:	:	:
D _b	3	DTRRLQKVN	DD-VEDEY	LVLFIP	23

RESULT 10
US-08-470-204A-30
; Sequence 30, Application US/08470204A
; Patent No. 6028247
; GENERAL INFORMATION:
; APPLICANT: Voelker, Toni Alois
; TITLE OF INVENTION: Plant Thioesterases
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Calgene, Inc.
; STREET: 1920 Fifth Street
; CITY: Davis
; STATE: California
; COUNTRY: USA
; ZIP: 95616
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB
; COMPUTER: Apple Macintosh IIfx
; OPERATING SYSTEM: Macintosh 7.1
; SOFTWARE: MicrosoftWord 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,204A
; FILING DATE: 06-JUN-95
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/824,247
; FILING DATE: 22-JAN-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/782,263
; FILING DATE: 24-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/773,096
; FILING DATE: 7-OCT-1991

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/704,861
;; FILING DATE: 21-MAY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US91/02960
;; FILING DATE: 25-APR-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/662,007
;; FILING DATE: 27-FEB-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/620,426
;; FILING DATE: 30-NOV-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/514,030
;; FILING DATE: 26-APR-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Elizabeth Lassen
;; REGISTRATION NUMBER: 31,845
;; NAME: Donna E. Scherer
;; REGISTRATION NUMBER: 34,719
;; REFERENCE/DOCKET NUMBER: CGNE 82-3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 916-753-6313
;; TELEFAX: 916-753-1510
;; INFORMATION FOR SEQ ID NO: 30:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-470-204A-30

Query Match 15.6%; Score 36.5; DB 3; Length 23;
Best Local Similarity 36.4%; Pred. No. 1.4e+02;
Matches 8; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 12 DLYRLEKLSRRYQDQAVLFIP 33
| |||::: |||
Db 3 DTRRLQKVND-VEDEYLVFIP 23

RESULT 11
US-08-840-713-40
; Sequence 40, Application US/08840713
; Patent No. 6498233
; GENERAL INFORMATION:
; APPLICANT: WELS, Winfried, Dr.
; APPLICANT: FOYMINAYA, Jesus
; TITLE OF INVENTION: NUCLEIC ACID TRANSFER SYSTEM
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 15th St., N.W., Suite 330 - G St. Lobby
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/840,713
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitts, Monica Chin
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: 1614-7014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638 - 5000
; TELEFAX: (202) 638 - 4810

;; INFORMATION FOR SEQ ID NO: 40:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-840-713-40

Query Match 15.4%; Score 36; DB 4; Length 12;
Best Local Similarity 63.6%; Pred. No. 75;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 17 EKLSSRRYQDQ 27
||| ||| |||
Db 1 EKLESSDYKDE 11

RESULT 12
US-10-038-612-54
; Sequence 54, Application US/10038612
; Patent No. 6723830
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively
; TITLE OF INVENTION: Modulate the Activity of Protein Kinases
; FILE REFERENCE: 1242.1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 35
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: FGFR-4
US-10-038-612-54

Query Match 15.4%; Score 36; DB 4; Length 35;
Best Local Similarity 63.6%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LRCQPPGVDL 13
||| ||| |||
Db 13 LRARRPPGPD 23

RESULT 13
US-09-865-621A-16
; Sequence 16, Application US/09865621A
; Patent No. 6555348
; GENERAL INFORMATION:
; APPLICANT: JORGENSEN, FLEMING
; APPLICANT: HANSEN, OLE CAI
; APPLICANT: STOUGAARD, PETER
; TITLE OF INVENTION: A NEW ENZYME ISOLATED FROM A BIFIDOBACTERIUM
; FILE REFERENCE: 02405.0200
; CURRENT APPLICATION NUMBER: US/09/865,621A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/207,154
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-865-621A-16

Query Match 15.4%; Score 36; DB 4; Length 44;
Best Local Similarity 23.3%; Pred. No. 3.8e+02;

	Matches	10;	Conservative	9;	Mismatches	16;	Indels	8;	Gaps	2;
Qy	5	CQGPPGVLYR----	LEKLSRRYQDQAVLFIPAMKRSLAGR	42						
Db	3	CYTSP---TYREKIALIDRLAERYKDHPALILWHISNEFEFG	42							

RESULT 14
US-09-865-621A-11
; Sequence 11, Application US/09865621A
; Patent No. 6555348
; GENERAL INFORMATION:
; APPLICANT: JORGENSEN, FLEMMING
; APPLICANT: HANSEN, OLE CAI
; APPLICANT: STOUGAARD, PETER
; TITLE OF INVENTION: A NEW ENZYME ISOLATED FROM A BIFIDOBACTERIUM
; FILE REFERENCE: 02405.0200
; CURRENT APPLICATION NUMBER: US/09/865,621A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 60/207,154
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-865-621A-11

Query Match	15.4%;	Score 36;	DB 4;	Length 46;
Best Local Similarity	34.6%;	Pred. NO. 4e+02;		
Matches 9;	Conservative	5;	Mismatches 12;	Indels 0;
Gaps 0;				

RESULT 15
 US-07-977-630-58
 ; Sequence 58, Application US/07977630
 ; Patent No. 5583038
 ; GENERAL INFORMATION:
 ; APPLICANT: Stover, Charles K.
 ; TITLE OF INVENTION: BACTERIAL EXPRESSION VECTORS CONTAINING
 ; DNA ENCODING SECRETION SIGNALS OF LIPOPROTEINS
 ; NUMBER OF SEQUENCES: 84
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi,
 ; ADDRESSEE: Stewart & Olstein
 ; STREET: 6 Becker Farm Road
 ; CITY: Roseland
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07068
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch diskette
 ; COMPUTER: IBM
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/977,630
 ; FILING DATE: No. 5583038ember 17, 1993
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Herron, Charles J.
 ; REGISTRATION NUMBER: 28,019
 ; REFERENCE/DOCKET NUMBER: 469201-174
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-994-1700
 ; TELEFAX: 201-994-1744
 ; INFORMATION FOR SEQ ID NO: 58:
 ; SEQUENCE CHARACTERISTICS:

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; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-977-630-58

Query Match          15.2%; Score 35.5; DB 1; Length 37;
Best Local Similarity 30.6%; Pred. No. 3.6e+02;
Matches 11; Conservative 6; Mismatches 14; Indels 5; Gaps

QY 14 YRLEKLSRRYQDQ-----AVLFIPAMKRSLAGRYR 44
      :|::|::|::|::|::|::|::|::|::|::|::|
DB 1 HELRSLARLYRNOIGDKFACELLGLGHKSDSMAARYR 36

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```

RESULT 16
US-07-934-656A-17
; Sequence 17, Application US/07934656A
; Patent No. 5500347
; GENERAL INFORMATION:
; APPLICANT: MOLL, Roland
; APPLICANT: FRANK, Werner W.
; TITLE OF INVENTION: PROCESS FOR THE PURIFICATION OF
; TITLE OF INVENTION: CYTOKERATIN 20 AND ITS USE FOR THE PRODUCTION OF
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaïdo, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,656A
; FILING DATE: 27-JAN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 23 945.4
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: P564-3003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-934-656A-17

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Query Match      15.0%; Score 35; DB 1; Length 22;
Best Local Similarity 43.8%; Pred. No. 2.2e+02;
Matches 7: Conservative 2; Mismatches 7; Indels 0; Gaps 0;

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RESULT 17
US-07-934-656A-18
; Sequence 18, Application US/07934656A
; Patent No. 5500347


```
;
; GENERAL INFORMATION:
; APPLICANT: MOLL, Roland
; APPLICANT: FRANK, Werner W.
; TITLE OF INVENTION: PROCESS FOR THE PURIFICATION OF
; TITLE OF INVENTION: CYTOKERATIN 20 AND ITS USE FOR THE PRODUCTION OF
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,656A
; FILING DATE: 27-JAN-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 40 23 945.4
; FILING DATE: 27-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,980
; REFERENCE/DOCKET NUMBER: P564-3003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-07-934-656A-18

Query Match 15.0%; Score 35; DB 1; Length 22;
Best Local Similarity 43.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 1 VTLCRCQPPGVLDLRL 16
| : ||||| :
Db 1 VNVEDAAPGVDLTRI 16

RESULT 18
US-09-828-645-7
; Sequence 7, Application US/09828645
; Patent No. 6743593
; GENERAL INFORMATION:
; APPLICANT: Hu, Yao Xiong
; TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
; FILE REFERENCE: 146-1-002
; CURRENT APPLICATION NUMBER: US/09/828,645
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 60/194,796
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: Xaa = L-carboxymethylcysteine
```

```
US-09-828-645-7

Query Match 15.0%; Score 35; DB 4; Length 30;
Best Local Similarity 36.8%; Pred. No. 3.3e+02;
Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 8 PPGVDLYRLKLSRRYQD 26
| ||| :| :
Db 12 PETTDLYXYEQLNDSSEE 30

RESULT 19
US-09-647-468-117
; Sequence 117, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 117
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of FR3 of versions "d", "d1" and "d3" of humanized H
; OTHER INFORMATION: chain V region
;
US-09-647-468-117

Query Match 15.0%; Score 35; DB 4; Length 32;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 18 KLSSRRYQDQAVLF 31
| : ||| :| :
Db 16 ELSSLRSEDSAVYF 29

RESULT 20
US-10-038-612-53
; Sequence 53, Application US/10038612
; Patent No. 6723830
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: Short Peptides Which Selectively
; TITLE OF INVENTION: Modulate the Activity of Protein Kinases
; FILE REFERENCE: 1242.1029-000 (CMCC-679)
; CURRENT APPLICATION NUMBER: US/10/038,612
; CURRENT FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 09/161,094
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 35
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: FGFR-3
;
US-10-038-612-53

Query Match 15.0%; Score 35; DB 4; Length 35;
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Best Local Similarity 60.0%; Pred. No. 4e+02; Mismatches 2; Indels 2; Gaps 0;

QY 3 LRCQGPBGVD 12
Db 13 LRARRPGLD 22

RESULT 21

US-09-574-377-30
; Sequence 30, Application US/09574377
; Patent No. 6573370
; GENERAL INFORMATION:
; APPLICANT: La Du, Bert
; TITLE OF INVENTION: PON3 And Uses Thereof
; FILE REFERENCE: UM-04408
; CURRENT APPLICATION NUMBER: US/09/574,377
; CURRENT FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; NAME/KEY: SITE
; LOCATION: (16)..(16)
; OTHER INFORMATION: Xaa at this position can be Asn or Pro.
; NAME/KEY: SITE
; LOCATION: (27)..(27)
; OTHER INFORMATION: Xaa at this position can be Asp or Val.
US-09-574-377-30

Query Match 15.0%; Score 35; DB 4; Length 45;
Best Local Similarity 27.8%; Pred. No. 5.5e+02;
Matches 5; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 6 QGPPGVLDYRLEKLSRR 23
Db 26 EXPPGSEVLRIQNVLSEK 43

RESULT 22

US-08-332-562A-22
; Sequence 22, Application US/08332562A
; Patent No. 5985599
; GENERAL INFORMATION:
; APPLICANT: MCKENZIE, Ian F.C.
; APPLICANT: HOGARTH, Mark P.
; APPLICANT: HIBBS, Margaret L.
; APPLICANT: SCOTT, Bernadette M.
; APPLICANT: BONADONNA, Lisa
; APPLICANT: HULETT, Mark D.
; TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,562A
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/896,457
; FILING DATE: 27-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 54270/119/GRHA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-332-562A-22

Query Match 14.7%; Score 34.5; DB 2; Length 45;
Best Local Similarity 33.3%; Pred. No. 6.5e+02;
Matches 12; Conservative 4; Mismatches 17; Indels 3; Gaps 2;

QY 11 VDLYRLEKLSRRYQDQAVLF-IPAMKRSLAGRYRC 45
Db 12 ISFFHNEK--SVRYHYSSNFSIPKANHSHSGDYVC 45

RESULT 23

US-08-480-190-180
; Sequence 180, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Storn
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
US-08-480-190-180
Query Match 14.5%; Score 34; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GPPGVDLYRLEK 18
Db 1 GPPKLDIRKEEK 12

RESULT 24
US-08-488-379-180
; Sequence 180, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-488-379-180
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Query Match 14.5%; Score 34; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GPPGVDLYRLEK 18
Db 1 GPPKLDIRKEEK 12
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RESULT 25

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US-08-475-399A-180
; Sequence 180, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.
; APPLICANT: Stern, Lawrence J.
; APPLICANT: Strominger, Jack L.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 276
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,399A
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: 15-JUN-1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: 11-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00246/168003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-507
; TELEFAX: 617/542-890
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 180:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-475-399A-180
Query Match 14.5%; Score 34; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GPPGVDLYRLEK 18
Db 1 GPPKLDIRKEEK 12

Search completed: October 31, 2005, 18:11:39
Job time : 45 secs
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OM protein - protein search, using sw model

Run on: October 31, 2005, 18:02:02 ; Search time 163 Seconds

(without alignments)
115.411 Million cell updates/sec

Title: US-09-503-387-3_COPY_44_88

Perfect score: 234

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Maximum DB seq length: 46

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
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- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	216	92.3	41	9	US-09-832-312-6
2	216	92.3	41	11	US-09-829-495-6
3	216	92.3	41	16	US-10-850-034-6
4	164	70.1	41	9	US-09-832-312-22
5	164	70.1	41	11	US-09-829-495-22
6	164	70.1	41	16	US-10-850-034-22
7	81	34.6	19	14	US-10-446-826-20
8	81	34.6	19	16	US-10-446-826-20
9	80	34.2	19	14	US-10-446-826-14
10	80	34.2	19	16	US-10-446-826-14
11	69	29.5	19	14	US-10-446-826-21
					Sequence 6, Appli
					Sequence 6, Appli
					Sequence 22, Appl
					Sequence 22, Appl
					Sequence 20, Appl
					Sequence 20, Appl
					Sequence 14, Appl
					Sequence 14, Appl
					Sequence 21, Appl

12	69	29.5	19	16	US-10-446-826-21	Sequence 21, Appl
13	50	21.4	30	14	US-10-040-862-10438	Sequence 10438, A
14	50	21.4	30	15	US-10-057-475B-10438	Sequence 10438, A
15	50	21.4	30	15	US-10-154-884B-10438	Sequence 10438, A
16	50	21.4	30	16	US-10-764-324-10438	Sequence 10438, A
17	50	21.4	34	14	US-10-040-862-9613	Sequence 9613, Ap
18	50	21.4	34	15	US-10-057-475B-9613	Sequence 9613, Ap
19	50	21.4	34	15	US-10-154-884B-9613	Sequence 9613, Ap
20	50	21.4	34	16	US-10-764-324-9613	Sequence 9613, Ap
21	49	20.9	15	20	US-11-111-953-330	Sequence 330, App
22	46.5	19.9	45	9	US-09-815-626-13	Sequence 13, Appl
23	46.5	19.9	45	9	US-09-822-687-7	Sequence 7, Appl
24	46.5	19.9	45	14	US-10-142-201B-4	Sequence 4, Appl
25	46.5	19.9	45	14	US-10-145-586-72	Sequence 72, Appl
26	46.5	19.9	45	14	US-10-145-586-83	Sequence 83, Appl
27	46.5	19.9	45	14	US-10-087-887-55	Sequence 55, Appl
28	46.5	19.9	45	14	US-10-098-871-66	Sequence 66, Appl
29	46.5	19.9	45	14	US-10-098-871-68	Sequence 68, Appl
30	46.5	19.9	45	15	US-10-004-378A-60	Sequence 60, Appl
31	46.5	19.9	45	15	US-10-038-854-113	Sequence 113, App
32	46.5	19.9	45	15	US-10-038-854-160	Sequence 160, App
33	46.5	19.9	45	15	US-10-038-854-161	Sequence 161, App
34	46.5	19.9	45	15	US-10-038-854-162	Sequence 162, App
35	45.5	19.4	37	10	US-09-892-877-396	Sequence 396, App
36	45.5	19.4	37	10	US-09-948-783-396	Sequence 396, App
37	45	19.2	35	16	US-10-425-115-364696	Sequence 364696,
38	45	19.2	44	14	US-10-384-850-12	Sequence 12, Appl
39	44.5	19.0	45	16	US-10-425-115-230569	Sequence 230569,
40	43	18.4	30	14	US-10-040-862-10439	Sequence 10439, A
41	43	18.4	30	15	US-10-057-475B-10439	Sequence 10439, A
42	43	18.4	30	15	US-10-154-884B-10439	Sequence 10439, A
43	43	18.4	30	16	US-10-764-324-10439	Sequence 10439, A
44	43	18.4	34	15	US-10-352-786-3933	Sequence 3933, Ap
45	43	18.4	35	15	US-10-352-786-4093	Sequence 4093, Ap
46	43	18.4	35	15	US-10-352-786-4125	Sequence 4125, Ap
47	43	18.4	36	15	US-10-352-786-4221	Sequence 4221, Ap
48	43	18.4	36	15	US-10-352-786-4253	Sequence 4253, Ap
49	43	18.4	36	15	US-10-352-786-4285	Sequence 4285, Ap
50	43	18.4	37	15	US-10-352-786-4317	Sequence 4317, Ap
51	43	18.4	37	15	US-10-352-786-4349	Sequence 4349, Ap
52	43	18.4	37	15	US-10-352-786-4381	Sequence 4381, Ap
53	43	18.4	38	15	US-10-352-786-4413	Sequence 4413, Ap
54	43	18.4	38	15	US-10-352-786-4445	Sequence 4445, Ap
55	43	18.4	39	15	US-10-352-786-9	Sequence 9, Appl
56	42.5	18.2	42	15	US-10-424-599-169292	Sequence 169292,
57	42	17.9	36	15	US-10-352-786-4301	Sequence 4301, Ap
58	42	17.9	37	15	US-10-352-786-4397	Sequence 4397, Ap
59	42	17.9	38	15	US-10-352-786-4461	Sequence 4461, Ap
60	42	17.9	39	15	US-10-352-786-25	Sequence 25, Appl
61	42	17.9	42	16	US-10-437-963-142322	Sequence 142322,
62	41.5	17.7	41	9	US-09-764-877-1139	Sequence 1139, Ap
63	41.5	17.7	41	15	US-10-242-515-1139	Sequence 1139, Ap
64	41	17.5	20	14	US-10-446-826-13	Sequence 13, Appl
65	41	17.5	20	16	US-10-446-826-13	Sequence 13, Appl
66	41	17.5	30	15	US-10-296-734-1392	Sequence 1392, Ap
67	41	17.5	30	18	US-10-792-582-148	Sequence 148, App
68	41	17.5	33	15	US-10-352-786-3709	Sequence 3709, Ap
69	41	17.5	34	15	US-10-352-786-3901	Sequence 3901, Ap
70	41	17.5	34	15	US-10-352-786-3937	Sequence 3937, Ap
71	41	17.5	35	15	US-10-352-786-4061	Sequence 4061, Ap
72	41	17.5	35	15	US-10-352-786-4097	Sequence 4097, Ap
73	41	17.5	35	15	US-10-352-786-4129	Sequence 4129, Ap
74	41	17.5	35	15	US-10-352-786-4141	Sequence 4141, Ap
75	41	17.5	36	15	US-10-352-786-4189	Sequence 4189, Ap
76	41	17.5	36	15	US-10-352-786-4225	Sequence 4225, Ap
77	41	17.5	36	15	US-10-352-786-4257	Sequence 4257, Ap
78	41	17.5	36	15	US-10-352-786-4269	Sequence 4269, Ap
79	41	17.5	36	15	US-10-352-786-4289	Sequence 4289, Ap
80	41	17.5	37	15	US-10-352-786-4321	Sequence 4321, Ap
81	41	17.5	37	15	US-10-352-786-4353	Sequence 4353, Ap
82	41	17.5	37	15	US-10-352-786-4365	Sequence 4365, Ap
83	41	17.5	37	15	US-10-352-786-4385	Sequence 4385, Ap
84	41	17.5	38	15	US-10-352-786-4417	Sequence 4417, Ap

RESULT 8
US-10-446-826-20
; Sequence 20, Application US/10446826
; Publication No. US20040152628A9
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOMASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
; FILE REFERENCE: 03459.0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 20
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-826-20

Query Match 34.6%; Score 81; DB 16; Length 19;
Best Local Similarity 89.5%; Pred. No. 0.00024;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 KLSSRYQDQAVLFIPAMK 36
||| ||||| ||||| |||||
Db 1 KLSSRYQDQAVLFIPMAK 19

RESULT 9
US-10-446-826-14
; Sequence 14, Application US/10446826
; Publication No. US20030186885A1
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOMASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
; FILE REFERENCE: 03459.0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-826-14

Query Match 34.6%; Score 81; DB 16; Length 19;
Best Local Similarity 89.5%; Pred. No. 0.00024;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 18 KLSSRYQDQAVLFIPAMK 36
||| ||||| ||||| |||||
Db 1 KLSSRYQDQAVLFIPMAK 19

US-10-446-826-14

Query Match 34.2%; Score 80; DB 14; Length 19;
Best Local Similarity 84.2%; Pred. No. 0.00033;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 KLSSRYQDQAVLFIPAMK 36
||| ||||| ||||| |||||
Db 1 KLDXXRYQDQAVLFIPAMK 19

RESULT 10
US-10-446-826-14
; Sequence 14, Application US/10446826
; Publication No. US20040152628A9
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOMASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
; FILE REFERENCE: 03459.0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(5)
; OTHER INFORMATION: Any amino acid
US-10-446-826-14

Query Match 34.2%; Score 80; DB 16; Length 19;
Best Local Similarity 84.2%; Pred. No. 0.00033;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 18 KLSSRYQDQAVLFIPAMK 36
||| ||||| ||||| |||||
Db 1 KLDXXRYQDQAVLFIPAMK 19

RESULT 11
US-10-446-826-21
; Sequence 21, Application US/10446826
; Publication No. US20030186885A1
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOMASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
; FILE REFERENCE: 03459.0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197

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; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(5)
; OTHER INFORMATION: Any amino acid
US-10-446-826-21

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Query Match 29.5%; Score 69; DB 14; Length 19;
Best Local Similarity 73.7%; Pred. No. 0.013;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 18 KLSSRYQDQAVLFIPAMK 36
Db 1 KLDDXXRYQDQAVLFIPMAK 19

RESULT 12
US-10-446-826-21
; Sequence 21, Application US/10446826
; Publication No. US20040152628A9
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOMASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF

```

Query Match      29.5%; Score 69; DB 16; Length 19;
Best Local Similarity 73.7%; Pred. No. 0.013;
Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy 18 KLSSRYQDQAVLFIPAMK 36
||| ||| ||| ||| ||| ||| ||| |||
Db 1 KLDXXRYQDQAVLFIPMAK 19

RESULT 13
US-10-040-862-10438
; Sequence 10438, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander

```

; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10438
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-040-862-10438

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Query Match 21.4%; Score 50; DB 14; Length 30;
Best Local Similarity 61.1%; Pred. No. 12;
Matches 11: Conservative 2; Mismatches 5; Indels

Qy	28	AVLFIPAMKRSLAGRYRC	45
Db	11	AELEIPAVKESDAGKYVC	28

RESULT 14
US-10-057-475B-10438
; Sequence 10438, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Me
; TITLE OF INVENTION: Hematological Mali
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057, 4
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186, 126
; PRIOR FILING DATE: 2000-03-01

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; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10438
; LENGTH: 30
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-057-475B-10438

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Query Match 21.4%; Score 50; DB 15; Length 30;
Best Local Similarity 61.1%; Pred. No. 12;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy	28	AVLFIPAMKRS	LAGRYRC	45
Db	11	AELEIPAVKES	DAGKYVC	28

RESULT 15
US-10-154-884B-10438
; Sequence 10438, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290

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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10438
; LENGTH: 30
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-154-884B-10438
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Query Match	21.4%;	Score 50;	DB 15;	Length 30;
Best Local Similarity	61.1%;	Pred. No. 12;		
Matches 11; Conservative	2;	Mismatches 5;	Indels 0;	Gaps 0;

Qy	28	AVLFIPAMKRS	LAGRYRC	45
Db	11	AELEIPAVKES	DAGKYIC	28

```

RESULT 16
US-10-764-324-10438
; Sequence 10438, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10438
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-10438

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Query Match	21.4%	Score 50;	DB 16;	Length 30;
Best Local Similarity	61.1%	Pred. NO. 12;		
Matches 11: Conservative	2;	Mismatches	5;	Indels 0; Gaps 0;

Qy	28	AVLFIPAMKRS	LAGRYC	45
Db	11	AELEIPAVKES	DAGKYC	28

RESULT 17
US-10-040-862-9613
; Sequence 9613, Application US/10040862
; Publication No. US20030078396A1

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; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9613
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-9613

Query Match      21.4%; Score 50; DB 14; Length 34;
Best Local Similarity 61.1%; Pred. No. 14;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      28 AVLFIAMKRSAGRYRC 45
Db      11 AELEIPAVKESDAGKYC 28

RESULT 18
US-10-057-475B-9613
; Sequence 9613, Application US/10057475B
; Publication No. US2004002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
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; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9613
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-9613

Query Match      21.4%; Score 50; DB 15; Length 34;
Best Local Similarity 61.1%; Pred. No. 14;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      28 AVLFIAMKRSAGRYRC 45
Db      11 AELEIPAVKESDAGKYC 28

RESULT 19
US-10-154-884B-9613
; Sequence 9613, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
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; Remaining Prior Application data removed - See File Wrapper or PALM.
;
; NUMBER OF SEQ ID NOS: 11290
;
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 9613
;
; LENGTH: 34
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
US-10-154-884B-9613

```

```
Query Match      21.4%; Score 50; DB 15; Length 34;
Best Local Similarity 61.1%; Pred. No. 14;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

Qy	28	AVLFIPAMKRS	LAGRYC	45
Dd	11	AELEIPAVKES	DAGKYC	28

RESULT 20

US-10-764-324-9613

; Sequence 9613, Application US/10764324

; Publication No. US20040175739A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for

; TITLE OF INVENTION: Hematological Malignancies

```

, FILE REFERENCE: 014058-0135200S
, CURRENT APPLICATION NUMBER: US/10/764,324
, CURRENT FILING DATE: 2004-01-23
, PRIOR APPLICATION NUMBER: US/10/040,862
, PRIOR FILING DATE: 2001-11-06
, PRIOR APPLICATION NUMBER: US 60/186,126
, PRIOR FILING DATE: 2000-03-01
, PRIOR APPLICATION NUMBER: US 60/190,479
, PRIOR FILING DATE: 2000-03-17
, PRIOR APPLICATION NUMBER: US 60/200,545
, PRIOR FILING DATE: 2000-04-27
, PRIOR APPLICATION NUMBER: US 60/202,302
, PRIOR FILING DATE: 2000-04-28
, PRIOR APPLICATION NUMBER: US 60/200,779
, PRIOR FILING DATE: 2000-04-28
, PRIOR APPLICATION NUMBER: US 60/200,999
, PRIOR FILING DATE: 2000-05-01
, PRIOR APPLICATION NUMBER: US 60/202,084
, PRIOR FILING DATE: 2000-05-04
, PRIOR APPLICATION NUMBER: US 60/206,201
, PRIOR FILING DATE: 2000-05-22
, PRIOR APPLICATION NUMBER: US 60/218,950
, PRIOR FILING DATE: 2000-07-14
, Remaining Prior Application data removed
, NUMBER OF SEQ ID NOS: 10467
, SOFTWARE: FastSeq for Windows Version 3.0
, SEQ ID NO 9613

```

```
Query Match      21.4%; Score 50; DB 16; Length 34;
Best Local Similarity 51.1%; Pred. NO. 14;
Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
```

Qy 28 AVLFIPAMKRSLAGRYRC 45
| | | | : | | | : |
Db 11 AELEIPAVKESDAGKYVC 28

RESULT 21
US-11-111-953-330

```

; Sequence 330, Application US/11111953
; Publication No. US20050214844A1
; GENERAL INFORMATION:
; APPLICANT: Moore et al.
; TITLE OF INVENTION: 86 Human Secreted Proteins
; FILE REFERENCE: PZ008P1C2
; CURRENT APPLICATION NUMBER: US/11/111,953
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: 10/219,793
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 09/209,462
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: PCT/US98/12125
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/049,547
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,548
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,549
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,550
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,566
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,606
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 60/049,607
; PRIOR FILING DATE: 1997-06-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 737

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Query Match	20.9%;	Score 49;	DB 20;	Length 15;
Best Local Similarity	57.1%;	Pred. No. 7.2;		
Matches	8;	Conservative	3;	Mismatches 3;
				Indels 0;
				Gaps 0;

67 CQGFPGVDTLRLK 18
|:|:|:|:|:|:
Db 1 CRGPGVGQTFRLR 14

```

RESULT 22
US-09-815-626-13
; Sequence 13, Application US/09815626
; Patent No. US20020076752A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; TITLE OF INVENTION: 33395, A NOVEL HUMAN LEUCINE-RICH REPEAT
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-031001
; CURRENT APPLICATION NUMBER: US/09/815,626
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/191,863
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-815-626-13

```

Query Match	19.9%;	Score 46.5;	DB 9;	Length 45;
Best Local Similarity	34.7%;	Pred. No. 63;		
Matches 17; Conservative	0;	Mismatches 19;	Indels 13;	Gaps 2;

RESULT 21
US-11-111-953-330

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 31, 2005, 17:55:59 ; Search time 38 Seconds
(without alignments)
113.941 Million cell updates/sec

Title: US-09-503-387-3_COPY_44_88
Perfect score: 234
Sequence: 1 VTLCQCPGVDLYRLEKLS.....DQAVLFIPAMKRSLAGRYRC 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 10717

Minimum DB seq length: 0
Maximum DB seq length: 46

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query			DB	ID	Description
	Score	Match	Length			
1	50	21.4	42	2	T07474	hypothetical prote
2	38	16.2	42	2	AD0269	hypothetical prote
3	36	15.4	39	2	B81912	hypothetical prote
4	35.5	15.2	40	2	JT0515	Ig heavy chain V-I
5	35	15.0	29	2	A05272	gelsolin, cytosoli
6	34	14.5	31	2	S49191	hypothetical prote
7	33.5	14.3	45	2	E95058	hypothetical prote
8	33	14.1	15	2	PH0772	T-cell receptor be
9	33	14.1	43	2	B57484	cell division cont
10	32.5	13.9	33	2	B58512	bromosleeper pepti
11	32	13.7	30	2	A56790	annexin, isoform P
12	32	13.7	36	2	S49315	MSL leader peptide
13	32	13.7	36	2	S45088	probable leader pe
14	32	13.7	36	2	A25028	erythromycin resis
15	32	13.7	39	2	F64718	hypothetical prote
16	32	13.7	43	2	S24180	histone H1.a, test
17	32	13.7	45	2	T07502	hypothetical prote
18	31.5	13.5	38	2	E95080	hypothetical prote
19	31	13.2	16	2	C49048	T-cell receptor be
20	31	13.2	33	2	B29541	big gastrin - Chin
21	31	13.2	39	2	A46662	collagen alpha 2(V
22	31	13.2	41	2	E82544	hypothetical prote
23	31	13.2	42	2	JT0516	Ig heavy chain V-I
24	31	13.2	43	2	S13581	collagen alpha 1(I
25	30.5	13.0	38	2	F82485	hypothetical prote
26	30.5	13.0	41	2	AH1890	hypothetical prote
27	30.5	13.0	45	2	F86607	L36 ribosomal prot
28	30.5	13.0	45	2	B72017	L36 ribosomal prot
29	30.5	13.0	45	2	F71470	probable L36 ribos

30	30	12.8	19	2	JP0057	ribosomal protein
31	30	12.8	20	2	JP0056	ribosomal protein
32	30	12.8	28	2	I60364	phosphorybosylpyro
33	30	12.8	31	2	A25629	cytochrome-c oxida
34	30	12.8	36	2	H82427	hypothetical prote
35	30	12.8	38	2	G70236	hypothetical prote
36	30	12.8	38	2	B47753	beta-defensin-11 -
37	30	12.8	39	2	B81897	hypothetical prote
38	30	12.8	41	2	S50091	DNA-directed DNA p
39	30	12.8	43	2	A37091	60K sialoprotein h
40	30	12.8	44	2	S77931	exoskeletal protei
41	30	12.8	45	2	AB0749	hypothetical prote
42	29.5	12.6	32	2	F90807	hypothetical prote
43	29.5	12.6	32	2	B85667	hypothetical prote
44	29.5	12.6	32	2	A64848	hypothetical prote
45	29.5	12.6	38	2	A05222	anthranilate phosp
46	29.5	12.6	38	2	A61070	pituitary adenylat
47	29.5	12.6	38	2	A49165	pituitary adenylat
48	29.5	12.6	40	2	S45688	glutathione transfe
49	29.5	12.6	41	2	T15832	hypothetical prote
50	29	12.4	12	2	PH1635	Ig H chain V-D-J r
51	29	12.4	18	4	I56393	lacZ/IS1 mutant fu
52	29	12.4	20	2	S50175	kallikrein (PK-120
53	29	12.4	24	2	B56978	collagen alpha 2(X
54	29	12.4	31	2	S03297	Ig alpha chain C r
55	29	12.4	31	2	S03295	Ig alpha chain C r
56	29	12.4	34	2	D81044	hypothetical prote
57	29	12.4	35	2	A64733	hypothetical prote
58	29	12.4	38	2	C82373	hypothetical prote
59	29	12.4	39	2	A38623	collagen alpha 1(I
60	29	12.4	41	2	S26936	Ig heavy chain V r
61	29	12.4	43	2	S11111	Ig heavy chain V r
62	29	12.4	44	2	PC2242	cytochrome c554 -
63	29	12.4	46	2	T42016	pp1-like Ser/Thr p
64	28.5	12.2	31	2	C82851	hypothetical prote
65	28.5	12.2	40	1	SWFGS	sauvagine - Sauvag
66	28.5	12.2	44	2	T19161	hypothetical prote
67	28	12.0	9	2	S26508	collagen alpha 2(V
68	28	12.0	12	2	A61360	vespakinin M - hor
69	28	12.0	18	2	S02175	acrosin (EC 3.4.21
70	28	12.0	20	2	JP0059	ribosomal protein
71	28	12.0	20	2	JP0060	ribosomal protein
72	28	12.0	20	2	JP0061	ribosomal protein
73	28	12.0	20	2	JU0330	hypothetical prote
74	28	12.0	20	2	A99091	hypothetical prote
75	28	12.0	21	2	S16073	alanine-tRNA ligase
76	28	12.0	23	2	JP0062	ribosomal protein
77	28	12.0	23	2	A61574	hyaluronic acid-bi
78	28	12.0	28	2	A60752	outer membrane pro
79	28	12.0	30	2	A31836	17K antigen - Rick
80	28	12.0	36	1	WISMAA	alpha-amylase inhi
81	28	12.0	37	2	AG0540	hypothetical prote
82	28	12.0	39	2	H82657	hypothetical prote
83	28	12.0	40	1	W4BP17	gene 4.1 protein -
84	28	12.0	40	2	T03831	hypothetical prote
85	28	12.0	41	2	G69484	hypothetical prote
86	28	12.0	43	2	B81995	hypothetical prote
87	28	12.0	43	2	E82246	hypothetical prote
88	27.5	11.8	27	2	A61071	pituitary adenylat
89	27.5	11.8	31	2	C95215	hypothetical prote
90	27.5	11.8	35	2	B95157	hypothetical prote
91	27.5	11.8	39	2	S00490	RNA-binding protei
92	27	11.5	8	2	PT0559	T-cell receptor be
93	27	11.5	10	2	S26506	collagen alpha 1(V
94	27	11.5	14	2	S00150	ovostatin - duck (
95	27	11.5	17	2	A27636	cytotoxin B - Clos
96	27	11.5	20	2	PQ0544	capsid protein VP5
97	27	11.5	21	2	A60225	pyruvate dehydroge
98	27	11.5	23	2	C56978	collagen alpha 1(I
99	27	11.5	24	2	T50123	peroxisomal target
100	27	11.5	26	2	S11629	elastin precursor

C;Species: Azotobacter vinelandii
C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S49191
R;Wientjens, R.; van Dongen, W.; Haaker, H.
submitted to the EMBL Data Library, April 1992
A;Description: Molecular cloning of fixA, fixB, fixC and fixX genes of Azotobacter vinelandii
A;Reference number: S49186
A;Accession: S49191
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-31 <WIE>
A;Cross-references: UNIPROT:Q44509; EMBL:X65515

Query Match 14.5%; Score 34; DB 2; Length 31;
Best Local Similarity 50.0%; Pred. No. 7.1e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 15 RLEKLSRRYQDQA 28
:|||||:|:|:|
Db 13 QLEKESARRYEELA 26

RESULT 7
E95058
hypothetical protein SP0504 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: E95058
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: E95058
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-45 <KUR>
A;Cross-references: UNIPROT:Q97S84; GB:AE005672; PIDN:AAK74662.1; PID:g14971977; GSPDB:G
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0504

Query Match 14.3%; Score 33.5; DB 2; Length 45;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 8; Conservative 6; Mismatches 7; Indels 3; Gaps 2;

QY 5 CQG--PPGVDLRLEKLSRRYQD 26
|||||:|:|:|:|:|
Db 14 CQGENPEDIEFYD-EQLQAEKVED 36

RESULT 8
PH0772
T-cell receptor beta chain (J4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0772
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0772
A;Molecule type: mRNA
A;Residues: 1-15 <CAS>
A;Cross-references: EMBL:X60866; NID:G52749; PIDN:CAA43256.1; PID:G52750
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 14.1%; Score 33; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 20 SSSRYQDQAVLP 31
|||:|||||
Db 3 SSRRDRDQAPLF 14

RESULT 9
B57484
cell division control protein CDC37 homolog splice form 2 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C;Accession: B57484
R;Grammatikakis, N.; Grammatikakis, A.; Yoneda, M.; Yu, Q.; Banerjee, S.D.; Toole, B.P.
J. Biol. Chem. 270, 16198-16205, 1995
A;Title: A novel glycosaminoglycan-binding protein is the vertebrate homologue of the cel
A;Reference number: A57484; MUID:95332325; PMID:7608185
A;Accession: B57484
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-43 <GRA>
A;Cross-references: UNIPROT:Q90653; GB:U25026
C;Keywords: alternative splicing

Query Match 14.1%; Score 33; DB 2; Length 43;
Best Local Similarity 34.5%; Pred. No. 1.4e+03;
Matches 10; Conservative 4; Mismatches 15; Indels 0; Gaps 0;

QY 1 VTLCQCGPPGVDLRLEKLSRRYQDQAV 29
| ||| ||| : |||
Db 1 VVQRCGCPVVGETHGQAGRASEHRDGAV 29

RESULT 10
B58512
bromosleeper peptide - cone shell (Conus radiatus)
C;Species: Conus radiatus (radial cone)
C;Date: 19-Mar-1997 #sequence_revision 11-Apr-1997 #text_change 16-Aug-2004
C;Accession: B58512
R;Craig, A.G.; Jimenez, E.C.; Dykert, J.; Nielsen, D.B.; Gulyas, J.; Abogadie, F.C.; Port
J. Biol. Chem. 272, 4689-4698, 1997
A;Title: A novel post-translational modification involving bromination of tryptophan. Ide
A;Reference number: A58512; MUID:97184108; PMID:9030520
A;Accession: B58512
A;Molecule type: protein
A;Residues: 1-33 <CRA>
A;Cross-references: UNIPROT:P58804
A;Note: author J.M. McIntosh confirmed by private communication that both modified prolin
C;Keywords: bromine; carboxyglutamic acid; hydroxyproline; toxin; venom
F;1/Modified site: 6-bromotryptophan (Trp) #status experimental
F;6,8,9,29/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental
F;21/Modified site: 4-hydroxyproline (Pro) #status atypical
F;22/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 13.9%; Score 32.5; DB 2; Length 33;
Best Local Similarity 63.6%; Pred. No. 1.2e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 VTLC-CQGP 10
||:|||||
Db 13 VTFKTCGPG 23

RESULT 11
A56790
annexin, isoform P34 - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: A56790
R;Smallwood, M.F.; Gurr, S.J.; McPherson, M.J.; Roberts, K.; Bowles, D.J.
Biochem. J. 281, 501-505, 1992
A;Title: The pattern of plant annexin gene expression.
A;Reference number: A56790; MUID:92143819; PMID:1736896

A;Accession: A56790
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-30 <SMA>
A;Cross-references: UNIPROT:Q40139; GB:X63996; GB:S79791; NID:g19173; PIDN:CAA45402.1; P
A;Note: sequence extracted from NCBI backbone (NCBIN:79791, NCBIP:79793)
C;Superfamily: annexin I; annexin repeat homology

Query Match 13.7%; Score 32; DB 2; Length 30;
Best Local Similarity 30.0%; Pred. No. 1.3e+03;
Matches 6; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 17 EKLSSSRYPDQAVLFIPAMK 36
|||:| | | :| :| :|
Db 1 EKISDKAYSDELIRILSIR 20
|||:| | | :| :| :|

RESULT 12
S49315
MSL leader peptide 1 - Enterococcus hirae
N;Alternate names: probable erythromycin resistance protein 1
C;Species: Enterococcus hirae
C;Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 18-Jun-1999
C;Accession: S49315
R;Raze, D.; Coyette, J.; Ghuysen, J.M.
submitted to the EMBL Data Library, September 1994
A;Reference number: S49315
A;Accession: S49315
A;Molecule type: DNA
A;Residues: 1-36 <RAZ>
A;Cross-references: EMBL:X81655; NID:g551433; PIDN:CAA57313.1; PID:g551434
A;Experimental source: strain S185
C;Superfamily: MSL leader peptide

Query Match 13.7%; Score 32; DB 2; Length 36;
Best Local Similarity 38.9%; Pred. No. 1.6e+03;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 16 LEKLSSSRYPDQAVLFIP 33
||:| :| | :| :|
Db 16 LKQTKNSDYADKYVRLIP 33
||:| :| | :| :|

RESULT 13
S45088
probable leader peptide erm1 - Streptococcus pyogenes plasmid pDB101 and pBT233
N;Alternate names: erm1 protein; erythromycin resistance protein erm1
C;Species: Streptococcus pyogenes
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Aug-2004
C;Accession: S45088; S68608
R;Ceglowski, P.; Boitsov, G.; Lueder, G.; Alonso, J.C.
submitted to the EMBL Data Library, June 1992
A;Reference number: S45072
A;Accession: S45088
A;Molecule type: DNA
A;Residues: 1-36 <CEG>
A;Cross-references: EMBL:X66468; NID:g496500; PIDN:CAA47094.1; PID:g496517
A;Experimental source: plasmid pDB101
A;Genetics: G1
R;Ceglowski, P.; Boitsov, A.; Chai, S.; Alonso, J.C.
Gene 136, 1-12, 1993
A;Title: Analysis of the stabilization system of pSM19035-derived plasmid pBT233 in Bac
A;Reference number: S68600; MUID:94123985; PMID:8293991
A;Accession: S68608
A;Molecule type: DNA
A;Residues: 1-36 <CE2>
A;Cross-references: EMBL:X64695; NID:g456362; PIDN:CAA45936.1; PID:g456371
A;Experimental source: plasmid pBT233
A;Genetics: G2
C;Genetics: <G1>
A;Gene: erm1
A;Genome: plasmid pDB101
C;Genetics: <G2>

A;Gene: erm1
A;Genome: plasmid pBT233

Query Match 13.7%; Score 32; DB 2; Length 36;
Best Local Similarity 38.9%; Pred. No. 1.6e+03;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 16 LEKLSSSRYPDQAVLFIP 33
||:| :| | :| :|
Db 16 LKQTKNSDYADKYVRLIP 33
||:| :| | :| :|

RESULT 14
A25028
erythromycin resistance protein, ORF1 - Enterococcus faecalis
N;Alternate names: macrolide-lincosamide-streptogramin B-resistance protein
C;Species: Enterococcus faecalis
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A25028
R;Shaw, J.H.; Clewell, D.B.
J. Bacteriol. 164, 782-796, 1985
A;Title: Complete nucleotide sequence of macrolide-lincosamide-streptogramin B-resistance
A;Reference number: A91808; MUID:86033641; PMID:2997130
A;Accession: A25028
A;Molecule type: DNA
A;Residues: 1-36 <SHA>
A;Cross-references: UNIPROT:P23130
C;Superfamily: unassigned leader peptides

Query Match 13.7%; Score 32; DB 2; Length 36;
Best Local Similarity 38.9%; Pred. No. 1.6e+03;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 16 LEKLSSSRYPDQAVLFIP 33
||:| :| | :| :|
Db 16 LKQTKNSDYADKYVRLIP 33
||:| :| | :| :|

RESULT 15
F64718
hypothetical protein HP1590 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: F64718
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: F64718
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-39 <TOM>
A;Cross-references: UNIPROT:O26108; GB:AE000656; GB:AE000511; NID:g2314771; PIDN:AA00862;

Query Match 13.7%; Score 32; DB 2; Length 39;
Best Local Similarity 53.3%; Pred. No. 1.7e+03;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 12 DLYRLEKLSSSRYPQD 26
|||:| :| | :| :|
Db 8 DLEFLKRLSSSDLKD 22
|||:| :| | :| :|

RESULT 16
S24180
histone H1.a, testis - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
C;Accession: S24180
R;Baubichon-Cortay, H.; Mallet, L.; Denoroy, L.; Roux, B.

Query Match 13.2%; Score 31; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QGPPG 10
| | | | |
Db 3 QGPPG 7

RESULT 22
E82544
hypothetical protein XF2541 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: E82544
R/anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: E82544
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-41 <SJM>
A/Cross-references: UNIPROT:Q9PAH7; GB:AE004061; GB:AE003849; NID:g9107747; PIDN:AAF8533
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorzy, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigretchado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.A.; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A/Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A/Reference number: A59328
A/Contents: annotation
C/Genetics:
A/Gene: XF2541

Query Match 13.2%; Score 31; DB 2; Length 41;
Best Local Similarity 52.6%; Pred. No. 2.5e+03;
Matches 10; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

QY 29 VLFIPAMKRSL--AGRYRC 45
| : | | | | | | | | |
Db 3 VVMIAAAVRSLLSAGRMWC 21

RESULT 23
JT0516
Ig heavy chain V-III region (JP12) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 30-May-1997
C/Accession: JT0516
R/Anker, R.; Conley, M.E.; Pollok, B.A.
J. Exp. Med. 169, 2109-2119, 1989
A/Title: Clonal diversity in the B cell repertoire of patients with X-linked agammaglobulinemia
A/Reference number: JT0511; MUID:89279157; PMID:2786547
A/Accession: JT0516
A/Molecule type: mRNA
A/Residues: 1-42 <ANK>
A/Note: the sequence shown here is one of eight productive V-D-J mu chain rearrangements
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/1-24/Domain: V region <VRE>
F/25-38/Domain: D region <DRE>
F/39-42/Domain: J region <JRE>

Query Match 13.2%; Score 31; DB 2; Length 42;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 18 KLSRRYQDQAVLF 31
: | | | | : | | | | :
Db 8 ELSSLRSEDTAVVY 21

RESULT 24
S13581
collagen alpha 1(IX) chain precursor, short splice form - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 15-Sep-2003
C/Accession: S13581; D35980
R/Muragaki, Y.; Kimura, T.; Ninomiya, Y.; Olsen, B.R.
Eur. J. Biochem. 192, 703-709, 1990
A/Title: The complete primary structure of two distinct forms of human alpha-1(IX) collagen
A/Reference number: S13580; MUID:91006164; PMID:2209617
A/Accession: S13581
A/Molecule type: mRNA
A/Residues: 1-43 <MUR>
A/Cross-references: EMBL:X54413; NID:g30087; PIDN:CAA38277.1; P/D:9A00#B
R/Muragaki, Y.; Nishimura, I.; Henney, A.; Ninomiya, Y.; Olsen, B.R.
Proc. Natl. Acad. Sci. U.S.A. 87, 2400-2404, 1990
A/Title: The alpha(IX) collagen gene gives rise to two different transcripts in both mouse and human
A/Reference number: A35980; MUID:90207204; PMID:1690886
A/Accession: D35980
A/Molecule type: DNA
A/Residues: 1-24 <MU2>
A/Cross-references: EMBL:M32133
C/Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C) are substituted by O-glycosylated.
C/Genetics:
A/Gene: GDB:COL9A1
A/Cross-references: GDB:119794; OMIM:120210
A/Map position: 6q12-6q14
A/Introns: 24/3
A/Complex: type IX collagen may be a heterotrimer of one alpha 1(IX) chain, one alpha 2(I) chain, and one alpha 3(I) chain.
C/Function:
A/Description: structural component of extracellular fibrous polymer associated with type I collagen in corneal epithelium the short splice form is predominantly produced.
A/Note: in corneal epithelium the short splice form is predominantly produced.
C/Keywords: alternative splicing; coiled coil; cornea; extracellular matrix; glycoprotein
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-43/Product: collagen alpha 1(IX) chain, short splice form (fragment) #status predicted
F/24-25/Domain: non-collagenous NC4 #status predicted <NC4>
F/26-43/Domain: collagenous COL3 (fragment) #status predicted <COL3>
F/24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

Query Match 13.2%; Score 31; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QGPPG 10
| | | | |
Db 31 QGPPG 35

RESULT 25
F82485
hypothetical protein VCA0234 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C/Accession: F82485
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.D.; Deusch, R.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dengui, J.; Sellers, P. L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: F82485
A/Status: preliminary
A/Molecule type: DNA

Search completed: October 31, 2005, 18:02:38
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 31, 2005, 17:55:59 ; Search time 173 Seconds
(without alignments)
133.200 Million cell updates/sec

Title: US-09-503-387-3_COPY_44_88
Perfect score: 234
Sequence: 1 VTLCQGPFGVDLYRLKLS.....DQAVLFIPAMKRSLAGRYRC 45

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 60209

Minimum DB seq length: 0
Maximum DB seq length: 46

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	22.2	36	2 Q6Q4B9	Q6q4b9 tagetes min
2	50	21.4	42	2 Q32948	Q32948 pinus thunb
3	41.5	17.7	35	2 Q8KYK6	Q8kyk6 bacillus an
4	41.5	17.7	35	2 Q6EZM2	Q6ezm2 bacillus an
5	41	17.5	41	2 Q64CY7	Q64cy7 uncultured
6	39.5	16.9	41	2 Q8EXK8	Q8exk8 leptospira
7	39.5	16.9	46	2 Q8VU04	Q8vu04 streptococc
8	39	16.7	32	2 Q725Z6	Q725z6 desulfovibr
9	38.5	16.5	42	2 Q8E8U0	Q8e8u0 shewanella
10	38	16.2	32	2 Q72FU1	Q72fu1 desulfovibr
11	38	16.2	39	2 Q70UV9	Q70uv9 myoxus glis
12	38	16.2	42	2 Q66AJ8	Q66aj8 yersinia ps
13	38	16.2	42	2 Q8ZEG3	Q8zeg3 yersinia pe
14	38	16.2	46	2 Q7S7T8	Q7s7t8 neurospora
15	37.5	16.0	46	2 Q70UI8	Q70ui8 uncultured
16	37	15.8	42	2 Q93305	Q93305 chaenocepha
17	37	15.8	42	2 Q93306	Q93306 chionodrac
18	36	15.4	25	2 Q70WF0	Q70wf0 aeromonas s
19	36	15.4	28	2 Q9TRM4	Q9trm4 bos taurus
20	36	15.4	37	2 Q732X8	Q732x8 bacillus ce
21	36	15.4	39	2 Q9JU98	Q9ju98 neisseria m
22	36	15.4	45	2 Q8L6S4	Q8l6s4 gossypium h
23	35.5	15.2	38	2 Q75W88	Q75w88 eriocheir j
24	35	15.0	29	2 Q7M2V6	Q7m2v6 oryctolagus
25	35	15.0	30	2 Q9R892	Q9r892 chlamydia t
26	35	15.0	37	2 Q8CLI7	Q8cli7 yersinia pe
27	35	15.0	40	2 Q9QWC8	Q9qwc8 rattus sp.
28	35	15.0	41	2 Q72A24	Q72a24 desulfovibr
29	35	15.0	43	2 Q9LI94	Q9li94 human papil
30	35	15.0	44	1 YL53 SCHPO	Q8tfg5 schizosacch
31	34.5	14.7	35	2 Q8F4R5	Q8f4r5 leptospira

32	34.5	14.7	45	2 Q83WQ0	Q83wq0 shigella bo
33	34	14.5	17	2 Q71UQ2	Q71uq2 homo sapien
34	34	14.5	32	2 Q44509	Q44509 azotobacter
35	34	14.5	39	2 Q05821	Q05821 saccharomyc
36	34	14.5	39	2 Q9PVG7	Q9pvq7 xiphophorus
37	34	14.5	43	2 Q7UUD2	Q7uud2 rhodopirell
38	34	14.5	45	2 Q7QV81	Q7qv81 giardia lam
39	33.5	14.3	41	2 Q69DR1	Q69dr1 drosophila
40	33.5	14.3	45	2 Q8L6G9	Q8l6g9 posidonio o
41	33.5	14.3	45	2 Q97S84	Q97s84 streptococc
42	33	14.1	31	2 Q73KQ7	Q73kq7 treponema d
43	33	14.1	32	2 Q7M6V2	Q7m6v2 mus musculu
44	33	14.1	35	2 Q7S2W2	Q7s2w2 neurospora
45	33	14.1	37	2 Q73DU6	Q73du6 bacillus ce
46	33	14.1	40	2 Q6NFR5	Q6nfr5 corynebacte
47	33	14.1	46	2 Q9QX77	Q9qx77 rattus norv
48	32.5	13.9	33	1 CXBW CONRA	P58804 conus radia
49	32.5	13.9	38	2 Q8IU36	Q8iu36 periplaneta
50	32.5	13.9	38	2 Q8IU37	Q8iu37 sepioteuthi
51	32.5	13.9	38	2 Q8IU38	Q8iu38 hydra magni
52	32.5	13.9	38	2 Q8IU39	Q8iu39 dugesia jap
53	32.5	13.9	38	2 Q75W94	Q75w94 halocynthia
54	32.5	13.9	38	2 Q75W87	Q75w87 oncorhynch
55	32.5	13.9	38	2 Q75W90	Q75w90 sardinops m
56	32.5	13.9	38	2 Q75W92	Q75w92 stephanolep
57	32.5	13.9	38	2 Q8AYP4	Q8ayp4 acipenser s
58	32.5	13.9	38	2 Q8AYP5	Q8ayp5 trachurus j
59	32	13.7	30	2 Q739F3	Q739f3 bacillus ce
60	32	13.7	32	2 Q9BPX8	Q9bpx8 homo sapien
61	32	13.7	35	2 Q8EB25	Q8eb25 shewanella
62	32	13.7	35	2 Q80017	Q80017 human immu
63	32	13.7	36	2 Q9UE39	Q9ue39 homo sapien
64	32	13.7	36	2 Q83U72	Q83u72 streptococc
65	32	13.7	36	2 Q83WK8	Q83wk8 enterococcu
66	32	13.7	36	2 Q77664	Q77664 human immu
67	32	13.7	37	2 Q49100	Q49100 mycoplasma
68	32	13.7	38	2 Q75W93	Q75w93 cyprinus ca
69	32	13.7	39	2 Q8TE27	Q8te27 homo sapien
70	32	13.7	39	2 Q26108	Q26108 helicobacte
71	32	13.7	40	2 Q62GT2	Q62gt2 burkholderi
72	32	13.7	40	2 Q8PCU1	Q8pcu1 xanthomonas
73	32	13.7	41	2 Q6C589	Q6c589 yarrowia li
74	32	13.7	42	2 Q7RCZ1	Q7rcz1 plasmodium
75	32	13.7	43	2 Q937G6	Q937g6 klebsiella
76	32	13.7	44	2 Q811V8	Q811v8 bacillus ce
77	32	13.7	44	2 Q87N11	Q87n11 vibrio para
78	32	13.7	45	2 Q32964	Q32964 pinus thunb
79	31.5	13.5	32	2 Q9TSQ0	Q9tsq0 cercopithe
80	31.5	13.5	38	2 Q97RU4	Q97ru4 streptococc
81	31.5	13.5	38	2 Q75W86	Q75w86 lampetra ja
82	31.5	13.5	39	2 Q9MZP7	Q9mzf7 bos taurus
83	31.5	13.5	41	2 Q6SF91	Q6sf91 uncultured
84	31.5	13.5	45	2 Q9NQ49	Q9nq49 homo sapien
85	31	13.2	16	2 Q9QUW5	Q9quw5 rattus sp.
86	31	13.2	20	2 Q9UWJ3	Q9uwj3 pyrococcus
87	31	13.2	23	2 Q9TWT9	Q9twj9 mytilus edu
88	31	13.2	31	2 Q9TWK5	Q9twk5 mytilus edu
89	31	13.2	31	2 Q9TT24	Q9tt24 sus scrofa
90	31	13.2	33	1 CAST_CHIBR	P10034 chinchilla
91	31	13.2	33	2 Q9TWD8	Q9twd8 carausius m
92	31	13.2	36	2 Q72WS2	Q72ws2 desulfovibr
93	31	13.2	37	2 Q8EIQ2	Q8eig2 shewanella
94	31	13.2	37	2 Q8EXV9	Q8exv9 leptospira
95	31	13.2	38	2 Q8CQ09	Q8cq09 staphylococ
96	31	13.2	39	2 Q8EGP4	Q8egp4 shewanella
97	31	13.2	41	2 Q9PAH7	Q9pah7 xylella fas
98	31	13.2	42	2 Q9T0Z2	Q9t0z2 bacterioph
99	31	13.2	42	2 Q50817	Q50817 mycobacteri
100	31	13.2	43	2 Q6WRF9	Q6wrf9 bos taurus

ALIGNMENTS

RP	SEQUENCE FROM N.A.
RR	STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX	MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA	Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA	Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.
RA	Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA	Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA	Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA	Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA	Xu J.-G., Zhao G.-P.;
RT	"Unique physiological and pathogenic features of <i>Leptospira</i>
RT	interrogans revealed by whole-genome sequencing.";
RL	Nature 422:888-893(2003).

NCBI_TaxID=882;
[1]
SEQUENCE FROM N.A.
DOI=10.1038/nbt959;
PubMed=15077118;
Heidelberg J.F., Seshadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R.,
Nelson W.C., Sullivan S.A., Fouts D.E., Haft D.H., Selengut J.,
Peterson J.D., Davidsen T.M., Zafar N., Zhou L., Radune D.,
Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R.,
Feldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.;
"The genome sequence of the anaerobic, sulfate-reducing bacterium
Desulfovibrio vulgaris Hildenborough.";


```
RC STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hannebusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauger L.J., Garcia E.;
RT "Insights into the genome evolution of Yersinia pestis through whole
RT genome comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
DR EMBL; BX936398; CAF21370.1; -.
KW Hypothetical protein.
SQ SEQUENCE 42 AA; 4690 MW; 4936841D8E98EE7E CRC64;

Query Match 16.2%; Score 38; DB 2; Length 42;
Best Local Similarity 35.3%; Pred. No. 1.1e+03;
Matches 6; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 10 GVDLYRLEKLSRRYQD 26
Db 12 GVDIYLMNQLTSTQVHE 28

RESULT 13
Q8ZEG3 PRELIMINARY; PRT; 42 AA.
AC Q8ZEG3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein YPO2210.
GN OrderedLocusNames=YPO2210;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414151; CAC91016.1; -.
DR PIR; AD0269; AD0269.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 42 AA; 4677 MW; C9E72F1D8E98EE62 CRC64;

Query Match 16.2%; Score 38; DB 2; Length 42;
Best Local Similarity 35.3%; Pred. No. 1.1e+03;
Matches 6; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 10 GVDLYRLEKLSRRYQD 26
Db 12 GVDIYLVNQLTSTQVRE 28

RESULT 14
Q7S7T8 PRELIMINARY; PRT; 46 AA.
ID Q7S7T8;
AC Q7S7T8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU04157.1;
OS Neurospora crassa.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000271; EAA32077.1; -.
SQ SEQUENCE 46 AA; 4780 MW; 9E9CE767B13820B0 CRC64;

Query Match 16.2%; Score 38; DB 2; Length 46;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 31 FIPAMKRSLAGRYR 44
Db 28 FLTMSISLVGRYR 41

RESULT 15
Q70UI8 PRELIMINARY; PRT; 46 AA.
ID Q70UI8;
AC Q70UI8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Laccase (EC 1.10.3.2) (Fragment).
GN Name=lac;
OS uncultured basidiomycete.
OC Eukaryota; Fungi; Basidiomycota; environmental samples.
OX NCBI_TaxID=175244;
RN [1]
RP SEQUENCE FROM N.A.
RA Luis P., Walther G., Kellner H., Martin F., Buscot F.;
RT "Diversity of laccase genes from basidiomycetes in a forest soil.";
RL Soil Biol. Biochem. 36:1025-1036(2004).
DR EMBL; AJ540275; CAD62538.1; -.
DR HSSP; Q9Y780; 1A65.
DR GO; GO:0008471; F:laccase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR008972; Cupredoxin.
KW Oxidoreductase.
FT NON_TER 1
FT NON_TER 46
SQ SEQUENCE 46 AA; 5430 MW; F104400E614C16B7 CRC64;

Query Match 16.0%; Score 37.5; DB 2; Length 46;
Best Local Similarity 31.8%; Pred. No. 1.5e+03;
Matches 7; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

QY 4 RCQGPFGVDL-YRLEKLSRRY 24
Db 21 QCEIIPGKSNMYRFQALQTGTF 42
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RESULT 16
O93305 ID O93305 PRELIMINARY; PRT; 42 AA.
AC O93305;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha globin (Fragment).
OS Chaeronocephalus aceratus (White crocodile fish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidei; Channichthyidae; Chaenocephalus.
OX NCBI_TaxID=36190;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278981; PubMed=9614073; DOI=10.1074/jbc.273.24.14745;
RA Zhao Y., Ratnayake-Lecamwasam M., Parker S.K., Cocco E.,
RA Camardella L., di Prisco G., Detrich H.W. III.;
RT "The major adult alpha-globin gene of antarctic teleosts and its
RT remnants in the hemoglobinless icefishes. Calibration of the
RT mutational clock for nuclear genes.";
RL J. Biol. Chem. 273:14745-14752(1998).
DR EMBL; AF049914; AAC25098.1; -.
DR HSSP; P45718; 1LA6.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0015671; P:oxygen transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000971; Globin.
DR InterPro; IPR009050; Globin_like.
DR Pfam; PF00042; Globin; 1.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT NON TER 1 1
SQ SEQUENCE 42 AA; 4734 MW; F499AE047E991E35 CRC64;

Query Match 15.8%; Score 37; DB 2; Length 42;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 31 FIPAMKRSLAGRYR 44
Db 29 FLSAVALSLADRYR 42

RESULT 17
O93306 ID O93306 PRELIMINARY; PRT; 42 AA.
AC O93306;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha globin (Fragment).
OS Chionodraco rastrispinosus (Ocellated icefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Notothenioidei; Channichthyidae; Chionodraco.
OX NCBI_TaxID=34790;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98278981; PubMed=9614073; DOI=10.1074/jbc.273.24.14745;
RA Zhao Y., Ratnayake-Lecamwasam M., Parker S.K., Cocco E.,
RA Camardella L., di Prisco G., Detrich H.W. III.;
RT "The major adult alpha-globin gene of antarctic teleosts and its
RT remnants in the hemoglobinless icefishes. Calibration of the
RT mutational clock for nuclear genes.";
RL J. Biol. Chem. 273:14745-14752(1998).
DR EMBL; AF049915; AAC25099.1; -.
DR HSSP; P45718; 1LA6.
DR GO; GO:0005344; F:oxygen transporter activity; IEA.
DR GO; GO:0015671; P:oxygen transport; IEA.
DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR000971; Globin.
DR InterPro; IPR009050; Globin_like.
DR Pfam; PF00042; Globin; 1.
DR PROSITE; PS01033; GLOBIN; 1.
KW Heme; Oxygen transport; Transport.
FT NON TER 1 1
SQ SEQUENCE 42 AA; 4734 MW; F499AE047E991E35 CRC64;

Query Match 15.8%; Score 37; DB 2; Length 42;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 31 FIPAMKRSLAGRYR 44
Db 29 FLSAVALSLADRYR 42

RESULT 18
Q70WF0 ID Q70WF0 PRELIMINARY; PRT; 25 AA.
AC Q70WF0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Aeromonas salmonicida.
OG Plasmid pAr-32.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=645;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ar-32;
RA Sorum H., L'Abée-Lund T.M., Solberg A., Wold A.;
RT "The integron containing IncU R plasmids pRAS1 and pAr-32 from the
RT fish pathogen Aeromonas salmonicida.";
RL Antimicrob. Agents Chemother. 47:1285-1290(2003).
DR EMBL; AJ517791; CAD57203.1; -.
KW Hypothetical protein; Plasmid.
FT NON TER 25 25
SQ SEQUENCE 25 AA; 2603 MW; 9D7CE3384EC26E9D CRC64;

Query Match 15.4%; Score 36; DB 2; Length 25;
Best Local Similarity 61.5%; Pred. No. 1.1e+03;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 33 PAMKRSLAGRYRC 45
Db 7 PVASRSLAVRPRC 19

RESULT 19
Q9TRM4 ID Q9TRM4 PRELIMINARY; PRT; 28 AA.
AC Q9TRM4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Vesicular amine transporter (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=93028536; PubMed=1357668;
RA Stern-Bach Y., Keen J.N., Bejerano M., Steiner-Mordoch S., Wallach M.,
RA Findlay J.B., Schuldiner S.;
RT "Homology of a vesicular amine transporter to a gene conferring
RT resistance to 1-methyl-4-phenylpyridinium.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:9730-9733(1992).
SQ SEQUENCE 28 AA; 3357 MW; A70D254C5C8A8346 CRC64;

Query Match 15.4%; Score 36; DB 2; Length 28;
Best Local Similarity 38.1%; Pred. No. 1.3e+03;
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 12 DLYRLEKLSRRYQDQAVLFI 32
Db 3 ELALLRRLQESRHSRXLILFI 23

RESULT 20

Q732X8
ID Q732X8 PRELIMINARY; PRT; 37 AA.
AC Q732X8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=BCE3782;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AE017276; AAS42687.1; -.
DR TIGR; BCE3782; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 37 AA; 4474 MW; 1F0AF43DD20620FE CRC64;

Query Match 15.4%; Score 36; DB 2; Length 37;
Best Local Similarity 31.0%; Pred. No. 1.8e+03;
Matches 9; Conservative 5; Mismatches 7; Indels 8; Gaps 1;

QY 5 CQGPVGVDLYRLEKLSRRYQDQAVLFI 33
Db 3 CEGN-----EKLOSTKKRVRVLFPP 23

RESULT 21

Q9JU98
ID Q9JU98 PRELIMINARY; PRT; 39 AA.
AC Q9JU98;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein NMA1426.
GN OrderedLocusNames=NMA1426;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491.";
RL Nature 404:502-506(2000).
DR EMBL; AL162755; CAB84665.1; -.
DR PIR; B81912; B81912.

KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 39 AA; 4347 MW; 78431A918706821C CRC64;
Query Match 15.4%; Score 36; DB 2; Length 39;
Best Local Similarity 47.4%; Pred. No. 1.9e+03;
Matches 9; Conservative 4; Mismatches 4; Indels 2; Gaps 1;

QY 16 LEKLSRR--YQDQAVLFI 32
Db 7 LRRLSGNRFYLDKAISFI 25

RESULT 22

Q8L6S4
ID Q8L6S4 PRELIMINARY; PRT; 45 AA.
AC Q8L6S4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MYB101 protein (Fragment).
GN Name=myb101;
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22941922; PubMed=14580676; DOI=10.1016/j.bbexp.2003.09.009;
RA Suo J., Liang X., Pu L., Zhang Y., Xue Y.;
RT "Identification of GhMYB109 encoding a R2R3 MYB transcription factor
RT that expressed specifically in fiber initials and elongating fibers of
RT cotton (Gossypium hirsutum L.).";
RL Biochim. Biophys. Acta 1630:25-34(2003).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 1 Myb-like domain.
DR EMBL; AJ459116; CAD30565.1; -.
DR HSSP; P06876; 1GV2.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR009057; Homeodomain like.
DR InterPro; IPR001005; Myb_DNA_binding.
DR Pfam; PF00249; Myb_DNA-binding; 1.
DR PROSITE; PS50090; MYB_3; 1.
KW Nuclear protein.
FT NON_TER 1
FT NON_TER 45
SQ SEQUENCE 45 AA; 5461 MW; 475F302957C492A6 CRC64;

Query Match 15.4%; Score 36; DB 2; Length 45;
Best Local Similarity 31.2%; Pred. No. 2.3e+03;
Matches 10; Conservative 4; Mismatches 6; Indels 12; Gaps 1;

QY 13 LYRLEKLSRRYQDQAVLFI 44
Db 24 IIRLHKLLGNRWS-----LIAGRYR 43

RESULT 23

Q7SW88
ID Q7SW88 PRELIMINARY; PRT; 38 AA.
AC Q7SW88;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Pituitary adenylate cyclase activating polypeptide (Fragment).
OS Eriocheir japonica (Japanese mitten crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Grapsoidea; Varunidae; Eriocheir.
OX NCBI_TaxID=95603;
RN [1]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 04:07:45 ; Search time 163 Seconds
(without alignments)
111.520 Million cell updates/sec

Title: US-09-503-387-3_COPY_134_180
Perfect score: 268
Sequence: 1 CQTRYGFDQFALYKEGPAP.....YRASFPITVTAAHSGTYRC 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 927287

Minimum DB seq length: 0
Maximum DB seq length: 48

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	268	100.0	47	4	AAB61259 Human TAN
2	268	100.0	47	6	ABU11225 Human TAN
3	220	82.1	47	4	AAB61272 Mouse TAN
4	220	82.1	47	6	ABU11238
5	47.5	17.7	42	3	AAB19610 Glucagon-
6	46.5	17.4	34	7	ADM34378 Human LY1
7	46.5	17.4	38	2	AAY20266 Human ubi
8	46.5	17.4	38	2	AAY20269 Human ubi
9	45.5	17.0	44	6	ABR83767 Pseudomon
10	45.5	17.0	44	7	ADF70087 Acma-type
11	45	16.8	24	6	ABB99764 Antigenic
12	45	16.8	30	7	ADM35220 Human LY1
13	45	16.8	41	7	ADM35348 Human LY1
14	44.5	16.6	45	4	AAU22223 Human car
15	44.5	16.6	45	7	ADE46191 Human car
16	44.5	16.6	45	8	ADJ07609 Human car
17	44	16.4	26	2	AAW22399 Soluble C
18	44	16.4	26	2	AAW75901 Recombina
19	44	16.4	26	8	ADS88820 Amino aci
20	44	16.4	30	2	AAV04273 Bovine va
21	44	16.4	42	5	ABG80828 Human SF-
22	43	16.0	13	8	ADI46793 Permeabil
23	43	16.0	13	8	ADI46809 Permeabil
24	43	16.0	13	8	ADP86970 Junctiona
25	43	16.0	13	8	ADP86986 Junctiona

26	43	16.0	14	8	ADI46794	Adi46794 Permeabil
27	43	16.0	14	8	ADI46810	Adi46810 Permeabil
28	43	16.0	14	8	ADP86971	Adp86971 Junctiona
29	43	16.0	14	8	ADP86987	Adp86987 Junctiona
30	43	16.0	17	8	ADI46788	Adi46788 Permeabil
31	43	16.0	17	8	ADI46804	Adi46804 Permeabil
32	43	16.0	17	8	ADP86965	Adp86965 Junctiona
33	43	16.0	17	8	ADP86981	Adp86981 Junctiona
34	43	16.0	19	8	ADI46789	Adi46789 Permeabil
35	43	16.0	19	8	ADI46805	Adi46805 Permeabil
36	43	16.0	19	8	ADP86982	Adp86982 Junctiona
37	43	16.0	19	8	ADP86966	Adp86966 Junctiona
38	43	16.0	28	2	AAW21973	Aaw21973 FCR pep1
39	43	16.0	28	2	AAW22247	Aaw22247 FCR pep 1
40	43	16.0	41	4	AAB61271	Aab61271 Mouse TAN
41	43	16.0	41	6	ABU11237	Abu11237 Mouse TAN
42	43	16.0	42	4	AAU21124	Aau21124 Human nov
43	43	16.0	42	5	ABG80829	Abg80829 Human SF-
44	43	16.0	43	2	AAR75862	Aar75862 Factor XI
45	42.5	15.9	21	5	AAU76481	Aau76481 Antioxi
46	42	15.7	12	8	ADI46792	Adi46792 Permeabil
47	42	15.7	12	8	ADI46808	Adi46808 Permeabil
48	42	15.7	12	8	ADP86985	Adp86985 Junctiona
49	42	15.7	12	8	ADP86969	Adp86969 Junctiona
50	42	15.7	15	8	ADI46803	Adi46803 Permeabil
51	42	15.7	15	8	ADI46787	Adi46787 Permeabil
52	42	15.7	15	8	ADP86980	Adp86980 Junctiona
53	42	15.7	15	8	ADP86964	Adp86964 Junctiona
54	42	15.7	30	4	ABB50698	Abb50698 Human sec
55	42	15.7	30	6	ABO44955	Abo44955 Novel hum
56	42	15.7	30	7	ABO26435	Abo26435 Protein a
57	41.5	15.5	39	4	AAU31439	Aau31439 Novel hum
58	41	15.3	21	8	ADG70460	Adg70460 Alginic a
59	41	15.3	26	2	AAV19726	Aay19726 SEQ ID NO
60	41	15.3	39	2	AAW74059	Aaw74059 Human hPE
61	41	15.3	46	5	ABG98308	Abg98308 Antibody
62	41	15.3	46	5	ABG98305	Abg98305 Antibody
63	40.5	15.1	26	2	AAV20272	Aay20272 Human ubi
64	40.5	15.1	35	4	AAU20373	Aam20373 Peptide #
65	40.5	15.1	35	4	ABB41004	Abb41004 Peptide #
66	40.5	15.1	35	4	AAU34779	Aam34779 Peptide #
67	40.5	15.1	35	4	ABB25097	Abb25097 Protein #
68	40.5	15.1	35	4	AAU74664	Aam74664 Human bon
69	40.5	15.1	35	4	AAU61863	Aam61863 Human bra
70	40.5	15.1	35	5	ABG44485	Abg44485 Human pep
71	40.5	15.1	45	2	AAV36531	Aay36531 Fragment
72	40.5	15.1	45	6	ADA12079	Ada12079 Human nov
73	40	14.9	13	8	ADI46745	Adi46745 Permeabil
74	40	14.9	13	8	ADI46729	Adi46729 Permeabil
75	40	14.9	14	8	ADI46730	Adi46730 Permeabil
76	40	14.9	14	8	ADI46746	Adi46746 Permeabil
77	40	14.9	17	8	ADI46740	Adi46740 Permeabil
78	40	14.9	17	8	ADI46724	Adi46724 Permeabil
79	40	14.9	19	8	ADI46725	Adi46725 Permeabil
80	40	14.9	19	8	ADI46741	Adi46741 Permeabil
81	40	14.9	21	5	ADK36472	Adk36472 Novel hum
82	40	14.9	21	8	ADR04108	Adr04108 Starch sy
83	40	14.9	24	5	ABP58996	Abp58996 Paenibaci
84	40	14.9	26	2	AAW00918	Aaw00918 Streptomy
85	40	14.9	26	3	AAV77199	Aay77199 S. venez
86	40	14.9	36	6	ABR62506	Abr62506 Modified
87	39.5	14.7	41	2	AAV48270	Aay48270 Human pro
88	39.5	14.7	43	6	ABM73011	Abm73011 Staphyloc
89	39.5	14.7	47	4	AAU92023	Aau92023 Human dig
90	39.5	14.7	47	4	AAU20001	Aau20001 Human liv
91	39.5	14.7	47	5	ABP40862	Abp40862 Human liv
92	39.5	14.7	47	7	ADJ14980	Adj14980 Human liv
93	39	14.6	12	8	ADI46744	Adi46744 Permeabil
94	39	14.6	12	8	ADI46728	Adi46728 Permeabil
95	39	14.6	15	8	ADI46723	Adi46723 Permeabil
96	39	14.6	15	8	ADI46739	Adi46739 Permeabil
97	39	14.6	47	2	AAW80351	Aaw80351 Sugi alle
98	38.5	14.4	26	3	AAU23988	Aab23988 Linker pe

99 38.5 14.4 30 7 ADM35219 Human LY1
100 38.5 14.4 35 6 ABR62513 Modified

Db 1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 47

ALIGNMENTS

RESULT 1
AAB61259
ID AAB61259 standard; protein; 47 AA.
XX
AC
XX
DT 04-APR-2001 (first entry)
XX
DE Human TANGO 268 Ig-like domain #2.

Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant; thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI; platelet membrane glycoprotein receptor; bleeding disorder; blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke; ischaemia; cardiovascular disease; immunological disease; liver disorder; cancer.

OS Homo sapiens.

XX WO200100810-A1.

PN 04-JAN-2001.

PD

XX 30-JUN-2000; 2000WO-US018152.

PF 30-JUN-1999; 99US-00345468.

PR 06-DEC-1999; 99US-00454824.

PR 14-FEB-2000; 2000US-00503387.

XX (MILL-) MILLENNIUM PHARM INC.

PA Busfield SJ, Villelall J, Jandrot-Perrus M, Vainchencker W;

XX Gill DS, Qian MD, Kingsbury G;

PI WPI; 2001-080877/09.

DR

XX New genes encoding human platelet-expressed collagen receptor,

XX glycoprotein VI, and its modulators, useful for preventing, treating and

PT diagnosing hemorrhagic disorders, thrombotic diseases and immunological

PT disorders.

PT

XX Disclosure; Page 203; 227pp; English.

PS

XX The present sequence is given in a specification relating to an isolated

CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor

CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides

CC and polypeptides and their modulators, e.g. antisense nucleic acids,

CC ribozymes and antibodies, are useful for preventing, treating and

CC diagnosing disorders associated with aberrant expression or activity of

CC GPVI. These disorders include bleeding disorders (e.g.

CC thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g.

CC thrombotic occlusion of the coronary arteries), haemorrhagic disorders,

CC coronary artery and cerebral artery diseases (e.g. stroke and ischaemia),

CC cardiovascular diseases (e.g. atherosclerosis and myocardial infarction),

CC immunological diseases (e.g. platelet disorder) and embryonic liver

CC disorders. Preferably they are used to prevent acture cardiac ischaemia

CC following angioplasty and metastatic cancers, especially of the colon and

CC liver

XX Sequence 47 AA;

SQ

Query Match 100.0%; Score 268; DB 4; Length 47;

Best Local Similarity 100.0%; Pred. No. 2.5e-28;

Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 47

RESULT 2
ABU11225
ID ABU11225 standard; peptide; 47 AA.
XX
AC ABU11225;
XX
DT 06-FEB-2003 (first entry)
XX
DE Human TANGO 268 Ig like domain #2.

Human; mouse; variable heavy; VH; antigen; cancer; complementarity determining region; TANGO 268; glycoprotein VI; GPVI; TANGO 268; extracellular matrix; collagen; platelet release; proliferation; migration; embryogenesis; inflammation; thrombosis; degranulation; thrombocytopaenia; antibody; thrombotic disorder; cerebral vascular disease; stroke; ischaemia; venous thromboembolism; leg swelling; pain; ulceration; pulmonary embolism; coronary disease; cardiovascular disease; angina pectoris; myocardial infarction; coronary restenosis; atherosclerosis; immunological disorder; developmental disorder; embryonic disorder; liver disorder; cerebral vascular disease; venous thromboembolism disease.

OS Homo sapiens.

XX WO200280968-A1.

PN 17-OCT-2002.

PD

XX 09-APR-2002; 2002WO-US011122.

PR 09-APR-2001; 2001US-00829495.

XX (MILL-) MILLENNIUM PHARM INC.

PA Busfield SJ, Villevall J, Jandrot-Perrus M, Vainchencker W;

XX Gill DS, Qian DM, Kingsbury G;

PI WPI; 2003-058477/05.

DR

XX Novel substantially purified antibody immunospecifically binding to TANGO

PT 268 antigen, useful for treating bleeding disorders such as

PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis.

PT

XX Disclosure; Page 212; 236pp; English.

PS

XX This invention relates to a novel purified antibody comprising a variable

CC heavy (VH) complementarity determining region (CDR)1, VH CDR2 or VH CDR3;

CC or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically

CC binding to a TANGO 268 (also referred as glycoprotein VI (GPVI)) antigen.

CC The antibodies of the invention act to decrease or block TANGO 268

CC binding to extracellular matrix components, or as a Collagen or platelet

CC release and aggregation blocker. The antibodies of the invention are

CC useful for modulating proliferation, migration, morphology,

CC differentiation and/or function of megakaryocytes and platelets,

CC including during development e.g. embryogenesis, modulating leukocyte-

CC platelet and platelet-endothelium interactions in inflammation and/or

CC thrombosis, and modulating platelet aggregation and degranulation. They

CC are also useful for modulating disorders associated with abnormal or

CC aberrant megakaryocyte and/or platelet proliferation, migration,

CC morphology, differentiation and/or function, e.g. bleeding disorders such

CC as thrombocytopaenia. Other diseases which may be modulated by these

CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.

CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases

CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);

CC coronary diseases (e.g. cardiovascular diseases including angina

CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,

CC etc); immunological disorders, developmental disorders, embryonic

CC disorders, liver disorders, cerebral vascular diseases, venous

CC thromboembolism disease, coronary diseases, and metastatic cancers. The

CC as thrombocytopaenia. Other diseases which may be modulated by these
CC antibodies are thrombotic disorders, cerebral vascular diseases (e.g.
CC stroke and ischaemia) venous thromboembolism diseases (e.g. diseases
CC involving leg swelling, pain and ulceration, pulmonary embolism, etc);
CC coronary diseases (e.g. cardiovascular diseases including angina
CC pectoris, myocardial infarction, coronary restenosis, atherosclerosis,
CC etc); immunological disorders, developmental disorders, embryonic
CC disorders, liver disorders, cerebral vascular diseases, venous
CC thromboembolism disease, coronary diseases, and metastatic cancers. The
CC antibodies of the invention only causes a transient decrease in platelet
CC counts, platelet aggregation, and/or platelet activation and so have some
CC advantages over prior art methods. The present sequence represents a
CC peptide sequence used to generate the antibodies of the invention
XX
SQ Sequence 47 AA;

Query Match 82.1%; Score 220; DB 6; Length 47;
Best Local Similarity 78.7%; Pred. No. 7.2e-22;
Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 47
||:| ||:||||| ||||:||||:|||||||
Db 1 CQSPYSFDFVLYKEGDTGPKRPEKWRANFPPIITVTAHSGTYRC 47

RESULT 5
AAB19610
ID AAB19610 standard; peptide; 42 AA.
XX
AC AAB19610;
XX
DT 22-JAN-2001 (first entry)
XX
DE Glucagon-like peptide 1 receptor N-terminal domain peptide 2.
XX
KW Glucagon-like peptide 1; G-coupled protein receptor; GLP-1R; vaccine;
KW metabolic disease; nervous system disorder;
KW extramembranous receptor domain; ERD; cancer.
XX
OS Unidentified.
XX
PN WO200053624-A1.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US006297.
XX
PR 11-MAR-1999; 99US-0124272P.
XX
PA (GRYP-) GRYPHON SCI.
XX
PI Kochendoerfer GG;
XX
DR WPI; 2000-572262/53.
XX
XX Producing a folded extramembranous receptor domain of a membrane receptor
PT under chemoselective chemical ligation conditions, useful as a vaccine
PT for treating various diseases, e.g. metabolic disease, nervous system
PT disorders and cancer.
XX
PS Example 1; Page 30; 56pp; English.
XX
CC Chemically synthesised peptide 2 is 1 of 3 peptides (see also AAB19609
CC and AAB19611) used in the preparation of the N-terminal domain (see
CC AAB19612) of glucagon-like peptide 1 receptor in an example of the method
CC of the invention. This relates to the chemical synthesis of
CC extramembranous receptor domains (ERDs), such as the soluble ligand-
CC binding extracellular and cytosolic domains, of membrane protein
CC receptors. The ERDs are produced by ligating, under chemoselective
CC ligation conditions, first and second peptides of an ERD of a membrane
CC protein receptor, where the peptides have unprotected chemoselective
CC reactive groups capable of forming a covalent bond. The ligation product
CC is exposed to a folding buffer having a chaotropic reagent and an organic

CC solvent that approximates the water-lipid interface of a cell membrane.
CC Exposure to the folding buffer is followed by isolation from the buffer
CC of ligation product that binds to a ligand of the membrane protein
CC receptor. The ligand-binding portion of the ligation product represents
CC folded ERD. The invention is exemplified by total chemical synthesis of
CC the N-terminal domain of glucagon-like peptide 1 receptor, demonstration
CC of its ability to bind to peptide ligand and characterisation of its
CC disulphide map. The method provides access to non-limiting amounts of
CC ultra-pure and ultra-homogeneous soluble ERDs useful for drug discovery,
CC high-throughput screening of receptor ligands, as therapeutics, e.g. for
CC treatment of metabolic diseases, nervous system diseases and cancer, and
XX as vaccines
XX
SQ Sequence 42 AA;

Query Match 17.7%; Score 47.5; DB 3; Length 42;
Best Local Similarity 34.8%; Pred. No. 97;
Matches 8; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Qy 7 FDQFALYKEGDPAPYKNPE-RWY 28
||:| ||:||||| ||||:||||:|||||||
Db 5 FDEYACWPDGEPGSGFVNVCWPY 27

RESULT 6
ADM34378
ID ADM34378 standard; peptide; 34 AA.
XX
AC ADM34378;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human LY1448P cancer related peptide for cancer detection method.
XX
KW cytostatic; T-cell vaccine; detection; cancer;
KW chronic lymphocytic leukemia.
XX
OS Homo sapiens.
XX
PN WO2003077836-A2.
XX
PD 25-SEP-2003.
XX
PF 06-NOV-2002; 2002WO-US035728.
XX
PR 06-NOV-2001; 2001US-00040862.
PR 23-MAY-2002; 2002US-00154884.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Algate PA, Mannion J, Retter M;
XX
DR WPI; 2003-756941/71.
XX
XX Detecting cancer in a patient comprises contacting a biological sample
PT from the patient with a binding agent that binds to a cancer-associated
PT polypeptide and comparing the amount of polypeptide to a predetermined
PT cutoff value.
XX
PS Disclosure; SEQ ID NO 9616; 419pp; English.
XX
CC The invention relates to a method of detecting (M1) cancer in a patient
CC by: (i) contacting a biological sample from the patient with an agent
CC that binds to any of three polypeptides given in the specification; (ii)
CC detecting in a sample an amount of the peptide that binds to the binding
CC agent; and (iii) comparing the amount of polypeptide present in the
CC patient's sample to a predetermined cutoff value. The specification also
CC discloses a separate method for detecting (M2) cancer in a patient by a
CC method similar to M1, except that the detection agent is an
CC oligonucleotide that binds to any of three polynucleotides given in the
CC specification. M1 and M2 are useful for detecting the presence of cancer
CC in a patient, especially chronic lymphocytic leukemia. The applicants
CC have identified specific human polypeptides overexpressed in one or more

CC types of hematological malignancies. This sequence corresponds to a
CC peptide used in the method of the invention.
XX
SQ Sequence 34 AA;

Query Match 17.4%; Score 46.5; DB 7; Length 34;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 30 ASFPITVTAAHSGTYRC 47
Db 12 ASFN-LSLTAHSGNYSC 28

RESULT 7
AAY20266
ID AAY20266 standard; protein; 38 AA.
XX
AC AAY20266;
XX
DT 22-JUL-1999 (first entry)
XX
DE Human ubiquitin B mutant protein fragment 5.
XX
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9845322-A2.
XX
PD 15-OCT-1998.
XX
PF 02-APR-1998; 98WO-IB000705.
XX
PR 10-APR-1997; 97US-0043163P.
XX
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
PA (UYUT-) RIJKSUNIV UTRECHT.
XX
PI Van Leeuwen FW, Grosveld FG, Burbach JPH;
XX
DR WPI; 1998-609901/51.
DR N-PSDB; AAX75755.
XX
PT Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also for
PT treatment and prevention with specific ribozymes or wild-type RNA.
XX
PS Disclosure; Fig 4; 258pp; English.
XX
CC This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC and many others listed) or susceptibility to these disorders. The method
CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the
CC used of neuronal system RNA molecules, specifically proteins including

CC beta-amyloid precursor protein (beta-APP), the microtubule associated
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC protein-C (HMGP-C) and neuroendocrine specific protein A
XX
SQ Sequence 38 AA;

Query Match 17.4%; Score 46.5; DB 2; Length 38;
Best Local Similarity 58.8%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 13 YKEG-DPAPYKNPERWY 28
Db 3 HPEGVDPAFGPASERWY 19

RESULT 8
AAY20269
ID AAY20269 standard; protein; 38 AA.
XX
AC AAY20269;
XX
DT 22-JUL-1999 (first entry)
XX
DE Human ubiquitin B mutant protein fragment 8.
XX
KW Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9845322-A2.
XX
PD 15-OCT-1998.
XX
PF 02-APR-1998; 98WO-IB000705.
XX
PR 10-APR-1997; 97US-0043163P.
XX
PA (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
PA (UYUT-) RIJKSUNIV UTRECHT.
XX
PI Van Leeuwen FW, Grosveld FG, Burbach JPH;
XX
DR WPI; 1998-609901/51.
DR N-PSDB; AAX75755.
XX
PT Diagnosing disease by detecting frameshift mutations in RNA or
PT corresponding protein mutations - used to diagnose cancer and
PT neurological diseases, particularly Alzheimer's disease, and also for
PT treatment and prevention with specific ribozymes or wild-type RNA.
XX
PS Disclosure; Fig 4; 258pp; English.
XX
CC This invention describes a novel method for the diagnosis of a disease
CC caused by, or associated with, an RNA molecule that has a frameshift
CC mutation. The method is used to diagnose age-related diseases, especially
CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II

CC and many others listed) or susceptibility to these disorders. The method
CC allows a definitive diagnosis of Alzheimer's disease in living patients,
CC at an early stage. It is based on the observation that disease may be
CC caused by mutations in RNA rather than DNA. The invention describes the
CC used of neuronal system RNA molecules, specifically proteins including
CC beta-amyloid precursor protein (beta-APP), the microtubule associated
CC proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC associated protein-2 (MAP2), neurofilament-L, neurofilament-M,
CC neurofilament-F, presenilin 1, presenilin II, glial fibrillary acidic
CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC protein-C (HMGP-C) and neuroendocrine specific protein A
XX
SQ Sequence 38 AA;

Query Match 17.4%; Score 46.5; DB 2; Length 38;
Best Local Similarity 58.8%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Qy 13 YKEG-DPAPYKNPERWY 28
Db 3 HPEGVDPAPGPASERWY 19

RESULT 9
ABR83767
ID ABR83767 standard; peptide; 44 AA.
XX
AC ABR83767;
XX
DT 15-OCT-2003 (first entry)
XX
DE Pseudomonas putida nlpD protein amino acids 44-87.
XX
KW Antibacterial; protozoacide; vaccine; cell-wall material; anchor protein;
KW Gram-positive bacterium; Lactococcus lactis; Acma; biocatalyst;
KW mucosal immunization; bioadsorbent; biofilter; microbiocatalyst;
KW vaccination; malaria; Streptococcus pneumoniae; fusion gene;
KW Streptococcus pneumoniae; protease maturation protein.
XX
OS Pseudomonas putida.
XX
PN WO2002101026-A2.
XX
PD 19-DEC-2002.
XX
PF 11-JUN-2002; 2002WO-NL000383.
XX
PR 11-JUN-2001; 2001EP-00202239.
XX
PA (NANO-) APPLIED NANOSYSTEMS BV.
XX
PI Leenhouts CJ, Ramasamy R, Steen A, Kok J, Buist G, Kuipers OP;
XX
DR WPI; 2003-167404/16.
XX
PT Improving binding of a proteinaceous substance e.g. an Acma-type protein
PT to a cell-wall material of microorganisms, comprises treating the
PT material with a solution capable of removing protein or carbohydrate from
PT the material.
XX
PS Example 3; Fig 24; 77pp; English.
XX
CC The invention relates to a method of obtaining cell-wall material of a
CC Gram-positive bacterium with improved capacity for binding to a
CC proteinaceous substance (PS), or binding PS to cell-wall material of the
CC bacterium, by treating the cell-wall material with a solution capable of
CC removing a cell-wall component such as a protein, (lipo)teichoic acid or
CC carbohydrate from the material. The method especially uses the binding of
CC the PS with an anchor protein from the cell wall of the organism. The
CC anchor protein is preferably the Lactococcus lactis Acma cell wall
CC binding domain or its homolog or functional derivative. The method is
CC useful for improving binding of proteinaceous substance to cell wall

CC material of gram-positive bacterium, e.g. for the preparation of a
CC pharmaceutical composition comprising a vaccine useful for mucosal
CC immunization and for preparing a biocatalyst. The preparation is also
CC useful for generating bioadsorbents or biofilters for environmental
CC purposes, microbiocatalysts and diagnostic tools. Also for vaccination
CC purposes, to elicit immunity for pathogens, like malaria and
CC Streptococcus pneumoniae. In an example of the invention, acid
CC pretreatment of Gram-positive bacteria to enhance binding of Acma protein
CC anchor fusion is investigated by the construction of a reporter plasmid
CC encoding a fusion gene of the L. lactis Acmd protein and the
CC Streptococcus pneumoniae protease maturation protein Ppma. This sequence
CC represents a homologue of the Lactococcus lactis Acma anchor protein. The
CC region can be used in the generation of the fusion protein of the
CC invention
XX
SQ Sequence 44 AA;

Query Match 17.0%; Score 45.5; DB 6; Length 44;
Best Local Similarity 52.2%; Pred. No. 1.9e+02;
Matches 12; Conservative 1; Mismatches 1; Indels 9; Gaps 2;

Qy 4 RYGFDOFALYKE-----GDPAPY 21
Db 15 RYGWD----YKELAARNGIPAPY 33

RESULT 10
ADF70087
ID ADF70087 standard; protein; 44 AA.
XX
AC ADF70087;
XX
DT 12-FEB-2004 (first entry)
XX
DE Acma-type homologue amino acid sequence.
XX
KW delivery; targeting system; Acma-type anchor protein; solid tumour;
KW health; medical; agricultural; cosmetic; controlled release.
XX
OS Pseudomonas putida.
XX
PN WO2003084508-A1.
XX
PD 16-OCT-2003.
XX
PF 04-APR-2003; 2003WO-NL000256.
XX
PR 04-APR-2002; 2002EP-00076316.
PR 04-APR-2002; 2002US-0369927P.
PR 05-APR-2002; 2002US-0370485P.
PR 20-DEC-2002; 2002EP-00080481.
XX
PA (NANO-) APPLIED NANOSYSTEMS BV.
XX
PI Friesen RHE, Leenhouts CJ, Hektor HJ, Van Esch JH, Heeres A;
PI Robillard GT;
XX
DR WPI; 2003-877005/81.
XX
PT Vehicle for targeted delivery of therapeutic or diagnostic agents,
PT includes protein anchor and system for inducing availability of the
PT agent.
XX
PS Example 3; Page 196; 303pp; English.
XX
CC The present invention describes a vehicle (A) for delivering a substance
CC (I) to a predetermined site, which comprises (I); a system for inducing
CC availability of at least one compartment of (A) towards the exterior;
CC and, as targeting system for directing (A) to the site, an Acma-type
CC anchor protein (II). (A) are used for delivery of diagnostic and
CC therapeutic agents to predetermined sites in the body, particularly
CC joints or solid tumours but can be used more generally for health,
CC medical, agricultural and cosmetic applications. (A) significantly

Db 4 LSLTAEHSGNYSC 16

RESULT 13
ADM35348
ID ADM35348 standard; peptide; 41 AA.
XX
AC ADM35348;
XX
DT 03-JUN-2004 (first entry)
XX
DE Human LY1448P cancer related peptide for cancer detection method.
XX
KW cytostatic; T-cell vaccine; detection; cancer;
KW chronic lymphocytic leukemia.
XX
OS Homo sapiens.
XX
PN WO2003077836-A2.
XX
PD 25-SEP-2003.
XX
PF 06-NOV-2002; 2002WO-US035728.
XX
PR 06-NOV-2001; 2001US-00040862.
PR 23-MAY-2002; 2002US-00154884.
XX
PA (CORI-) CORIXA CORP.
XX
PI Gaiger A, Algate PA, Mannion J, Retter M;
XX
DR WPI; 2003-756941/71.
XX
PT Detecting cancer in a patient comprises contacting a biological sample
PT from the patient with a binding agent that binds to a cancer-associated
PT polypeptide and comparing the amount of polypeptide to a predetermined
PT cutoff value.
XX
PS Disclosure; SEQ ID NO 11154; 419pp; English.
XX
CC The invention relates to a method of detecting (M1) cancer in a patient
CC by: (i) contacting a biological sample from the patient with an agent
CC that binds to any of three polypeptides given in the specification; (ii)
CC detecting in a sample an amount of the peptide that binds to the binding
CC agent; and (iii) comparing the amount of polypeptide present in the
CC patient's sample to a predetermined cutoff value. The specification also
CC discloses a separate method for detecting (M2) cancer in a patient by a
CC method similar to M1, except that the detection agent is an
CC oligonucleotide that binds to any of three polynucleotides given in the
CC specification. M1 and M2 are useful for detecting the presence of cancer
CC in a patient, especially chronic lymphocytic leukemia. The applicants
CC have identified specific human polypeptides overexpressed in one or more
CC types of hematological malignancies. This sequence corresponds to a
CC peptide used in the method of the invention.
XX
SQ Sequence 41 AA;

Query Match 16.8%; Score 45; DB 7; Length 41;
Best Local Similarity 53.8%; Pred. No. 2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 35 ITVTAHSGTYRC 47
:::|||||
Db 3 LSLTAEHSGNYSC 15

RESULT 14
AAU22223
ID AAU22223 standard; protein; 45 AA.
XX
AC AAU22223;
XX
DT 18-DEC-2001 (first entry)
XX

KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
KW cardiovascular disorder; angiogenic disorder; kidney disorder;
KW gastrointestinal disorder; pregnancy-related disorder;
KW endocrine disorder.

XX
OS Homo sapiens.
XX
PN US2003059908-A1.
XX
PD 27-MAR-2003.
XX
PF 07-MAR-2002; 2002US-00091504.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 22-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 23-AUG-2000; 2000US-0227182P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.

PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.

PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764869.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Barash SC;
XX
XX
DR WPI; 2003-743766/70.
DR N-PSDB; ADE45576.
XX
PT New cardiovascular system related polynucleotides and polypeptides,
PT useful for preventing, treating, or ameliorating a medical condition,
PT such as cancer of cardiovascular tissues and cancer metastases.
XX
PS Claim 11; SEQ ID NO 997; 262pp; English.
XX
CC The invention relates to human cardiovascular system related polypeptides
CC and the polynucleotides encoding them. The polypeptides, polynucleotides
CC and antibodies to the polypeptides are useful for diagnosing a
CC pathological condition or a susceptibility to a pathological condition,
CC for preventing, treating, or ameliorating a medical condition, such as
CC cancer of cardiovascular system tissues, proliferative disorders, foetal
CC and developmental abnormalities, haematopoietic disorders, diseases of
CC the immune system, AIDS, autoimmune diseases (e.g., rheumatoid
CC arthritis), inflammation, allergies, neurological disorders (e.g.,
CC Alzheimer's disease, Parkinson's disease), cognitive disorders,
CC schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis,
CC diabetes, atherosclerosis, cardiovascular disorders, angiogenic
CC disorders, kidney disorders, gastrointestinal disorders, pregnancy-
CC related disorders, endocrine disorders and infections. The nucleic acids
CC are also useful for chromosome identification, radiation hybrid mapping
CC or long-range restriction mapping. The polypeptides and polynucleotides
CC may also be used as food additives or preservatives to increase or
CC decrease storage capabilities, fat content or other nutritional
CC components. This sequence represents a human cardiovascular system
CC related polypeptide of the invention.
XX
SQ Sequence 45 AA;

Query Match 16.6%; Score 44.5; DB 7; Length 45;
Best Local Similarity 38.5%; Pred. No. 2.7e+02;
Matches 15; Conservative 1; Mismatches 12; Indels 11; Gaps 2;

QY 9 QFALYKEGDPAFYKNPERWYRASFPFIITVTAHSGTYRC 47
Db 1 QFLLDKLGPD-----MVTASIPLI--TGVHSGKNRC 28

RESULT 16
ADJ07609
ID ADJ07609 standard; protein; 45 AA.
XX
AC ADJ07609;
XX
DT 04-NOV-2004 (first entry)
XX
DE Human cardiovascular system associated polypeptide SeqID997.
XX
KW autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;
KW breast neoplasms; liver neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; cerebral ischaemia;
KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; skin aging; sunburn;
KW organ transplantation; cell culture; tissue regeneration; chemotaxis;
KW food additive; preservative; cardiovascular system associated antigen;
KW nuclear factor kappaB; NFkappaB; promoter element; human.
XX
OS Homo sapiens.
XX

PN US2004005575-A1.
XX
PD 08-JAN-2004.
XX
PF 26-AUG-2002; 2002US-00227577.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.

PR	29-SEP-2000;	2000US-0236327P.	XX	Rosen CA, Ruben SM, Barash SC;
PR	29-SEP-2000;	2000US-0236367P.	PI	
PR	29-SEP-2000;	2000US-0236368P.	XX	
PR	29-SEP-2000;	2000US-0236369P.	DR	WPI; 2004-081713/08.
PR	29-SEP-2000;	2000US-0236370P.	DR	N-PSDB; ADJ06994.
PR	02-OCT-2000;	2000US-0236802P.	XX	
PR	02-OCT-2000;	2000US-0237037P.	PT	New cardiovascular system-related nucleic acid molecule, useful for
PR	02-OCT-2000;	2000US-0237038P.	PT	diagnosing, preventing or treating diseases of the cardiovascular system,
PR	02-OCT-2000;	2000US-0237039P.	PT	and in chromosome mapping, drug screening or in pharmacogenomics.
PR	02-OCT-2000;	2000US-0237040P.	XX	
PR	13-OCT-2000;	2000US-0239935P.	PS	Claim 11; SEQ ID NO 997; 262pp; English.
PR	13-OCT-2000;	2000US-0239937P.	XX	
PR	20-OCT-2000;	2000US-0240960P.	CC	The invention relates to an isolated nucleic acid molecule encoding a
PR	20-OCT-2000;	2000US-0241221P.	CC	human cardiovascular system associated polypeptide (or antigens), Or its
PR	20-OCT-2000;	2000US-0241785P.	CC	fragment. Also included recombinant vectors, recombinant host cells, an
PR	20-OCT-2000;	2000US-0241786P.	CC	isolated human cardiovascular system associated polypeptide (including
PR	20-OCT-2000;	2000US-0241787P.	CC	its fragment, allelic variant, species homologue or epitope), an isolated
PR	20-OCT-2000;	2000US-0241808P.	CC	antibody that binds specifically to a human cardiovascular system
PR	20-OCT-2000;	2000US-0241809P.	CC	associated polypeptide, diagnosing a pathological condition or
PR	20-OCT-2000;	2000US-0241826P.	CC	susceptibility to a pathological condition (comprising determining the
PR	01-NOV-2000;	2000US-0244617P.	CC	presence or absence of a mutation in human cardiovascular system
PR	08-NOV-2000;	2000US-0246474P.	CC	associated nucleic acid and diagnosing a condition based on the presence
PR	08-NOV-2000;	2000US-0246475P.	CC	or absence of the mutation), identifying a binding partner to human
PR	08-NOV-2000;	2000US-0246476P.	CC	cardiovascular system associated polypeptides, the gene corresponding to
PR	08-NOV-2000;	2000US-0246477P.	CC	the human cardiovascular system associated cDNA sequence and identifying
PR	08-NOV-2000;	2000US-0246478P.	CC	an activity in a biological assay comprising expressing the human
PR	08-NOV-2000;	2000US-0246523P.	CC	cardiovascular system associated cDNA in a cell, isolating the
PR	08-NOV-2000;	2000US-0246524P.	CC	supernatant, detecting an activity in a biological assay and identifying
PR	08-NOV-2000;	2000US-0246525P.	CC	the protein in the supernatant having the activity. The human
PR	08-NOV-2000;	2000US-0246526P.	CC	cardiovascular system associated nucleic acids and polypeptides are used
PR	08-NOV-2000;	2000US-0246527P.	CC	to prevent, treat or ameliorate a medical condition (for example in
PR	08-NOV-2000;	2000US-0246528P.	CC	humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep), for
PR	08-NOV-2000;	2000US-0246532P.	CC	example autoimmune diseases such as rheumatoid arthritis,
PR	08-NOV-2000;	2000US-0246609P.	CC	hyperproliferative disorders, for example neoplasms of the breast or
PR	08-NOV-2000;	2000US-0246610P.		
PR	08-NOV-2000;	2000US-0246611P.		
PR	08-NOV-2000;	2000US-0246613P.		
PR	17-NOV-2000;	2000US-0249207P.		
PR	17-NOV-2000;	2000US-0249208P.		
PR	17-NOV-2000;	2000US-0249209P.		
PR	17-NOV-2000;	2000US-0249210P.		
PR	17-NOV-2000;	2000US-0249211P.		
PR	17-NOV-2000;	2000US-0249212P.		
PR	17-NOV-2000;	2000US-0249213P.		
PR	17-NOV-2000;	2000US-0249214P.		
PR	17-NOV-2000;	2000US-0249215P.		
PR	17-NOV-2000;	2000US-0249216P.		
PR	17-NOV-2000;	2000US-0249217P.		
PR	17-NOV-2000;	2000US-0249218P.		
PR	17-NOV-2000;	2000US-0249244P.		
PR	17-NOV-2000;	2000US-0249245P.		
PR	17-NOV-2000;	2000US-0249264P.		
PR	17-NOV-2000;	2000US-0249265P.		
PR	17-NOV-2000;	2000US-0249297P.		
PR	17-NOV-2000;	2000US-0249299P.		
PR	01-DEC-2000;	2000US-0249300P.		
PR	01-DEC-2000;	2000US-0250160P.		
PR	05-DEC-2000;	2000US-0250391P.		
PR	05-DEC-2000;	2000US-0251030P.		
PR	05-DEC-2000;	2000US-0251988P.		
PR	05-DEC-2000;	2000US-0256719P.		
PR	06-DEC-2000;	2000US-0251479P.		
PR	08-DEC-2000;	2000US-0251856P.		
PR	08-DEC-2000;	2000US-0251868P.		
PR	08-DEC-2000;	2000US-0251869P.		
PR	08-DEC-2000;	2000US-0251989P.		
PR	08-DEC-2000;	2000US-0251990P.		
PR	11-DEC-2000;	2000US-0254097P.		
PR	05-JAN-2001;	2001US-0259678P.		
PR	17-JAN-2001;	2001US-00764869.		
PR	07-MAR-2002;	2002US-00091504.		
XX				
PA	(HUMA-) HUMAN GENOME SCI INC.			

Query Match

Best Local Similarity

Matches 15; Conservative 1; Mismatches 12; Indels 11; Gaps 2;

16.6%; Score 44.5; DB 8; Length 45;

38.5%; Pred. No. 2.7e+02;

QY

9 QFALYKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 47

||| ||| ||| :| | ||| ||

Db

1 QFLDLKLGp-----MVTASIPLI--TGVHSGKNRC 28

||| ||| ||| :| | ||| ||

RESULT 17

AAW22399

ID AAW22399 standard; peptide; 26 AA.

XX AAW22399;

XX 08-OCT-1997 (first entry)

XX Soluble CD14 protein amino acids 143-168.

XX Soluble; CD14; glycoposphoinositol anchored membrane protein; infection;

KW cell surface; neutrophil; lipopolysaccharide; bacterium; interleukin;

KW tumour necrosis factor-alpha; growth; invasiveness; pathogenic; monocyte;

KW dissemination; bloodstream; peritoneal cavity; bacteraemia; antagonist;

KW gastrointestinal tract; septicaemia; appendicitis; gastroenteritis;

XX inflammatory bowel disease; peritonitis.

OS Homo sapiens.

XX WO9700081-A1.

PN 03-JAN-1997.

XX 19-JUN-1996; 96WO-US010803.

PF 19-JUN-1995; 95US-00491759.

XX (GOYE/) GOYERT S M.

XX

Query Match 16.4%; Score 44; DB 8; Length 26;
Best Local Similarity 21.7%; Pred. No. 1.6e+02;
Matches 5; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 25 ERWYRASFPPIITVTAHSGTYRC 47
: : | : : : : | | | : |
Db 4 QQWLKPGULKVLSIAQAHSLNFSC 26

RESULT 20
AAY04273
ID AAY04273 standard; peptide; 30 AA.

XX AC AAY04273;
XX DT 17-JUN-1999 (first entry)
XX DE

XX DE Bovine vascular smooth muscle cell growth factor peptide #9.

XX KW Vascular smooth muscle cell growth factor; VSGF; diagnosis; psoriasis;
XX KW wound healing; intractable skin ulcer; diabetic retinopathy;
XX KW rheumatoid arthritis; angiomas; arteriosclerosis; solid tumour;
XX KW abnormal blood vessel forming disease by fibroblast growth factor.

XX OS Bos sp.
XX PN EP905235-A2.
XX PD 31-MAR-1999.
XX PF 13-AUG-1998; 98EP-00115264.
XX PR 13-AUG-1997; 97JP-00218491.
XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PI Yamasaki M, Shibata K, Hanai N, Furuya A;
XX DR WPI; 1999-206772/18.

XX PT New vascular smooth growth factor gene and polypeptide useful as
XX PT diagnostic agents and for healing wounds and prevention of abnormal blood
XX PT vessels.

XX PS Example 2; Page 27; 36pp; English.

XX CC The present sequence represents a bovine vascular smooth muscle growth
XX CC factor (VSGF) peptide. VSGF polypeptides, antigenic portions of and anti-
XX CC VSGF antibodies are useful as diagnostic agents for detecting disease
XX CC related to abnormal blood vessel formation. VSGF polypeptides are also
XX CC useful for healing wounds or for preventing formation of an abnormal
XX CC blood vessel. Inhibiting activity of a recombinant human VSGF against
XX CC vascular formation induced by basic fibroblast factor (bFGF) was shown by
XX CC injection of VSGF and bFGF into rat cornea. After 3 days vascular
XX CC formation was clearly inhibited. Anti-VSGF antibodies are also useful for
XX CC detection of wound healing failure, intractable skin ulcers, diabetic
XX CC retinopathy, psoriasis, rheumatoid arthritis, angiomas, arteriosclerosis,
XX CC arteriosclerosis or solid tumours

XX SQ Sequence 30 AA;

Query Match 16.4%; Score 44; DB 2; Length 30;
Best Local Similarity 53.3%; Pred. No. 1.9e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 4 RYGFDDQFALYKEGDP 18
| : : : | | | |
Db 16 REGYTEFSLRVEGDP 30

RESULT 21
ABG80828

ID ABG80828 standard; protein; 42 AA.

XX AC ABG80828;

XX DT 29-NOV-2002 (first entry)

XX DE Human SF-A mutant protein R199A.

XX KW Scaffold protein; C-type lectin-like domain; CTLD; alpha-helix;
XX KW beta-strand; connecting segment; 14loop region; tetranectin;
XX KW ligand-binding specificity; human; mouse; rat; chicken; mutant; mutein.

XX OS Homo sapiens.
XX OS Synthetic.

XX PN WO200248189-A2.

XX PD 20-JUN-2002.

XX PF 13-DEC-2001; 2001WO-DK000825.

XX PR 13-DEC-2000; 2000DK-00001872.

XX PR 28-FEB-2001; 2001US-0272098P.

XX PA (BORE-) BOREAN PHARMA AS.

XX PI Etzerodt M, Holtet TL, Graversen NJH, Thogersen HC;

XX DR WPI; 2002-643278/69.

XX PT Protein comprising a variant of model C-type lectin-like domains (CTLD),
XX PT in which alpha helices, beta-strands, connecting segments are conserved
XX PT to maintain CTLD scaffold structure, while the loop region is altered.

XX PS Claim 1; Page 17; 168pp; English.

XX CC The present invention relates to a new protein with scaffold structure of
XX CC C-type lectin-like domains (CTLD). The invention comprises a variant of a
XX CC model CTLD where alpha-helices and beta-strands and connecting segments
XX CC are conserved such that scaffold structure of C-type lectin-like domains
XX CC (CTLD) is substantially maintained, while the 14loop region is altered by
XX CC amino acid substitution, deletion, insertion or their combination. The
XX CC invention is useful for preparing a library of nucleotide sequences
XX CC encoding related proteins by randomising part or all of the nucleic acid
XX CC sequence encoding the loop region of its CTLD. The artificial CTLD
XX CC protein products are preferable to antibody derivatives as each binding
XX CC site is a single structurally autonomous protein domain. When used as
XX CC components of compositions to be used for in vivo diagnostic or
XX CC therapeutic purposes, artificial CTLD protein products constructed on the
XX CC basis of human CTLDs are virtually identical to the corresponding natural
XX CC CTLD protein already present in the body and are therefore less
XX CC immunogenic to the patient. They also have a smaller size, and thus
XX CC provide tissue penetration and distribution, as well as shorter half life
XX CC in circulation. Since murine and human tetranectin are identical in
XX CC structure, straightforward swapping of polypeptide segments defining
XX CC ligand-binding specificity between murine and human tetranectin
XX CC derivatives may be achieved. The present amino acid sequence represents a
XX CC mutant protein of the invention

XX SQ Sequence 42 AA;

Query Match 16.4%; Score 44; DB 5; Length 42;
Best Local Similarity 31.4%; Pred. No. 2.9e+02;
Matches 11; Conservative 3; Mismatches 11; Indels 10; Gaps 2;

Qy 13 YKEGDPAPYKNPERWYRASFPPIITVTAHSGTYRC 47
| : | | | | | | | | : | : |
Db 15 YSDGTPVNYTN---WYRGE-----PAGAGKEQC 39

RESULT 22
ADI46793
ID ADI46793 standard; peptide; 13 AA.

XX AC ADI46793;
XX XX
DT 06-MAY-2004 (first entry)
XX XX
DE Permeabilising peptide of human JAM-1 SeqID502.
XX XX
KW mucosal delivery; permeabilising peptide;
KW mucosal epithelial paracellular transport; epithelial junction;
KW epithelial membrane adhesive protein; junctional adhesion molecule; JAM;
KW occludin; claudin; sexual dysfunction; male erectile sexual dysfunction;
KW female sexual dysfunction; human.
XX XX
OS Homo sapiens.
XX XX
PN WO2004003145-A2.
XX XX
PD 08-JAN-2004.
XX XX
PF 24-JUN-2003; 2003WO-US019994.
XX XX
PR 28-JUN-2002; 2002US-0392512P.
XX XX
PA (NAST-) NASTECH PHARM CO INC.
XX XX
PI Quay SC;
XX XX
DR WPI; 2004-091087/09.
XX XX
PT Composition comprising biologically active agent and permeabilizing
PT peptide that reversibly enhances mucosal epithelial paracellular
PT transport by modulating epithelial junctional structure and/or physiology
PT in mammal.
XX XX
PS Disclosure; SEQ ID NO 502; 426pp; English.
XX XX
CC This invention relates to a novel composition comprising a biologically
CC active agent and mucosal delivery-enhancing effective amount of
CC permeabilising peptide that reversibly enhances mucosal epithelial
CC paracellular transport by modulating epithelial junctional structure
CC and/or physiology in a mammal. The agent of the invention inhibits
CC homotypic binding of epithelial membrane adhesive protein chosen
CC junctional adhesion molecule (JAM), occludin and claudin. The
CC biologically active agent is effective for treatment of sexual
CC dysfunction, for example male erectile sexual dysfunction or female
CC sexual dysfunction. The present sequence is that of a permeabilising
CC peptide of human JAM-1 which may be used during the production of the
CC composition of the invention.
XX XX
SQ Sequence 13 AA;
Query Match 16.0%; Score 43; DB 8; Length 13;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 36 TVTAAHSGTYRC 47
Db :||| |||||
1 SVTREDSTGYRC 12
RESULT 23
ADI46809
ID ADI46809 standard; peptide; 13 AA.
XX XX
AC ADI46809;
XX XX
DT 06-MAY-2004 (first entry)
XX XX
DE Permeabilising peptide of human JAM-1 SeqID518.
XX XX
KW mucosal delivery; permeabilising peptide;
KW mucosal epithelial paracellular transport; epithelial junction;
KW epithelial membrane adhesive protein; junctional adhesion molecule; JAM;
KW epithelial membrane adhesive protein; junctional adhesion molecule; JAM;

KW occludin; claudin; sexual dysfunction; male erectile sexual dysfunction;
KW female sexual dysfunction; human.
XX XX
OS Homo sapiens.
XX XX
PN WO2004003145-A2.
XX XX
PD 08-JAN-2004.
XX XX
PF 24-JUN-2003; 2003WO-US019994.
XX XX
PR 28-JUN-2002; 2002US-0392512P.
XX XX
PA (NAST-) NASTECH PHARM CO INC.
XX XX
PI Quay SC;
XX XX
DR WPI; 2004-091087/09.
XX XX
PT Composition comprising biologically active agent and permeabilizing
PT peptide that reversibly enhances mucosal epithelial paracellular
PT transport by modulating epithelial junctional structure and/or physiology
PT in mammal.
XX XX
PS Disclosure; SEQ ID NO 518; 426pp; English.
XX XX
CC This invention relates to a novel composition comprising a biologically
CC active agent and mucosal delivery-enhancing effective amount of
CC permeabilising peptide that reversibly enhances mucosal epithelial
CC paracellular transport by modulating epithelial junctional structure
CC and/or physiology in a mammal. The agent of the invention inhibits
CC homotypic binding of epithelial membrane adhesive protein chosen
CC junctional adhesion molecule (JAM), occludin and claudin. The
CC biologically active agent is effective for treatment of sexual
CC dysfunction, for example male erectile sexual dysfunction or female
CC sexual dysfunction. The present sequence is that of a permeabilising
CC peptide of human JAM-1 which may be used during the production of the
CC composition of the invention.
XX XX
SQ Sequence 13 AA;
Query Match 16.0%; Score 43; DB 8; Length 13;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 36 TVTAAHSGTYRC 47
Db :||| |||||
1 SVTREDSTGYRC 12
RESULT 24
ADP86970
ID ADP86970 standard; peptide; 13 AA.
XX XX
AC ADP86970;
XX XX
DT 09-SEP-2004 (first entry)
XX XX
DE Junctional adhesion molecule 1 (JAM-1) peptide seqid 375.
XX XX
KW anorectic; cytostatic; eating disorder; neuroprotective; nootropic;
KW cachexia; intranasal composition; peptide YY; obesity; cancer;
KW malnutrition; wasting; Alzheimer's disease; colon adenocarcinoma;
KW pancreatic adenocarcinoma; breast carcinoma; cachexia; cancer cachexia;
KW junctional adhesion molecule 1; JAM-1; epithelial junction; human.
XX XX
OS Homo sapiens.
XX XX
PN US2004115135-A1.
XX XX
PD 17-JUN-2004.
XX XX
PF 17-DEC-2002; 2002US-00322266.

XX 17-DEC-2002; 2002US-003222266.
PR (QUAY/) QUAY S C.
XX Quay SC;
PI WPI; 2004-478989/45.
XX Intranasal compositions for treating obesity, cancer, or malnutrition or
PT wasting related to cancer, comprises peptide compound(s) formulated for
PT mucosal delivery to mammalian subject.
XX Disclosure; SEQ ID NO 375; 86pp; English.
XX The invention describes an intranasal composition comprising peptide YY
CC compound(s) formulated for mucosal delivery to a mammalian subject. Also
CC described is a kit for treatment of a mammalian subject comprising the
CC intranasal composition of peptide compound(s). The composition is used
CC for treating obesity, cancer, or malnutrition or wasting related to
CC cancer in the subject. It is used to alleviate Alzheimer's disease, colon
CC adenocarcinoma, pancreatic adenocarcinoma, breast carcinoma, treatment
CC and prevention of malnutrition resulting from iatrogenic causes or
CC cachexia associated with advanced disease, or cancer cachexia in the
CC subject. The composition alleviates the symptoms without unacceptable
CC adverse side effects. This is the amino acid sequence of a human
CC junctional adhesion molecule 1 (JAM-1) that may be used in a composition
CC of the invention to modulate epithelial junction structure and/or
CC physiology.
XX Sequence 13 AA;
SQ Query Match 16.0%; Score 43; DB 8; Length 13;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 36 TVTAAHSGTYRC 47
Db 1 SVTREDSGTYRC 12
RESULT 25
ADP86986
ID ADP86986 standard; peptide; 13 AA.
XX AC ADP86986;
XX DT 09-SEP-2004 (first entry)
XX DE Junctional adhesion molecule 1 (JAM-1) peptide seqid 391.
XX KW anorectic; cytostatic; eating disorder; neuroprotective; nootropic;
KW cachexia; intranasal composition; peptide YY; obesity; cancer;
KW malnutrition; wasting; Alzheimer's disease; colon adenocarcinoma;
KW pancreatic adenocarcinoma; breast carcinoma; cachexia; cancer cachexia;
KW junctional adhesion molecule 1; JAM-1; epithelial junction; human.
XX OS Homo sapiens.
XX PN US2004115135-A1.
XX PD 17-JUN-2004.
XX PF 17-DEC-2002; 2002US-003222266.
XX PR 17-DEC-2002; 2002US-003222266.
XX PA (QUAY/) QUAY S C.
XX PI Quay SC;
XX DR WPI; 2004-478989/45.
XX

PT Intranasal compositions for treating obesity, cancer, or malnutrition or
PT wasting related to cancer, comprises peptide compound(s) formulated for
PT mucosal delivery to mammalian subject.
XX Disclosure; SEQ ID NO 391; 86pp; English.
XX The invention describes an intranasal composition comprising peptide YY
CC compound(s) formulated for mucosal delivery to a mammalian subject. Also
CC described is a kit for treatment of a mammalian subject comprising the
CC intranasal composition of peptide compound(s). The composition is used
CC for treating obesity, cancer, or malnutrition or wasting related to
CC cancer in the subject. It is used to alleviate Alzheimer's disease, colon
CC adenocarcinoma, pancreatic adenocarcinoma, breast carcinoma, treatment
CC and prevention of malnutrition resulting from iatrogenic causes or
CC cachexia associated with advanced disease, or cancer cachexia in the
CC subject. The composition alleviates the symptoms without unacceptable
CC adverse side effects. This is the amino acid sequence of a human
CC junctional adhesion molecule 1 (JAM-1) that may be used in a composition
CC of the invention to modulate epithelial junction structure and/or
CC physiology.
XX Sequence 13 AA;
SQ Query Match 16.0%; Score 43; DB 8; Length 13;
Best Local Similarity 66.7%; Pred. No. 91;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 36 TVTAAHSGTYRC 47
Db 1 SVTREDSGTYRC 12

Search completed: October 29, 2005, 04:24:10
Job time : 170 secs

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OM protein - protein search, using sw model

Run on: October 29, 2005, 04:18:41 ; Search time 42 Seconds
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Searched: 513545 seqs, 74649064 residues

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	220	82.1	47	3	US-09-414-453A-23
5	46.5	17.4	38	2	US-08-726-306A-119
6	46.5	17.4	38	2	US-08-726-306A-122
7	46	17.2	42	2	US-08-476-866-23
8	44	16.4	26	1	US-08-254-095-1
9	44	16.4	30	4	US-09-132-769-17
10	43	16.0	28	3	US-09-043-731-13
11	43	16.0	41	3	US-09-345-468-22
12	43	16.0	41	3	US-09-414-453A-22
13	43	16.0	45	2	US-08-332-562A-22
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15	41	15.3	39	4	US-09-443-780C-57
16	41	15.3	39	4	US-09-079-723-41
17	40.5	15.1	26	2	US-08-726-306A-125
18	40.5	15.1	43	2	US-08-332-562A-21
19	40	14.9	36	4	US-10-027-038-5
20	39	14.6	36	2	US-08-251-472-10
21	39	14.6	36	3	US-09-248-082-10
22	38.5	14.4	35	4	US-10-027-038-14
23	38.5	14.4	36	4	US-10-027-038-11
24	38	14.2	33	4	US-09-763-331-7
25	38	14.2	45	2	US-08-332-562A-27
26	37	13.8	15	1	US-08-230-047-34
27	36.5	13.6	48	4	US-09-023-905A-18

28	36	13.4	31	3	US-09-556-876-11	Sequence 11, Appl
29	36	13.4	34	2	US-08-454-236-6	Sequence 6, Appli
30	36	13.4	35	2	US-08-332-562A-126	Sequence 126, App
31	36	13.4	47	4	US-09-270-767-44894	Sequence 44894, A
32	36	13.4	47	4	US-09-270-767-60362	Sequence 60362, A
33	35	13.1	15	4	US-09-142-524D-97	Sequence 97, Appl
34	35	13.1	15	4	US-09-142-524D-160	Sequence 160, App
35	35	13.1	18	2	US-08-374-652C-89	Sequence 89, Appl
36	35	13.1	18	2	US-08-374-652C-91	Sequence 91, Appl
37	35	13.1	21	2	US-08-454-236-9	Sequence 9, Appli
38	35	13.1	24	1	US-08-484-635-114	Sequence 114, App
39	35	13.1	24	2	US-08-484-631-114	Sequence 114, App
40	35	13.1	24	2	US-08-827-570-114	Sequence 114, App
41	35	13.1	26	4	US-09-369-247-170	Sequence 170, App
42	35	13.1	31	2	US-08-809-440-16	Sequence 16, Appl
43	35	13.1	31	3	US-08-822-324-12	Sequence 12, Appl
44	35	13.1	32	4	US-09-563-222C-139	Sequence 139, App
45	35	13.1	35	2	US-08-473-475A-23	Sequence 23, Appl
46	35	13.1	36	3	US-09-439-897-65	Sequence 65, Appl
47	35	13.1	38	2	US-08-809-440-15	Sequence 15, Appl
48	35	13.1	44	4	US-09-716-129-75	Sequence 75, Appl
49	35	13.1	46	1	US-07-676-647-4	Sequence 4, Appli
50	35	13.1	46	1	US-08-449-329-4	Sequence 4, Appli
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52	35	13.1	46	2	US-08-585-258-4	Sequence 4, Appli
53	35	13.1	46	3	US-09-211-590-4	Sequence 4, Appli
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55	35	13.1	47	2	US-08-809-440-17	Sequence 17, Appl
56	34.5	12.9	20	4	US-09-449-064A-29	Sequence 29, Appl
57	34.5	12.9	38	4	US-09-673-395A-372	Sequence 372, App
58	34.5	12.9	43	4	US-10-018-865-30	Sequence 30, Appl
59	34.5	12.9	44	2	US-08-559-492-13	Sequence 13, Appl
60	34	12.7	10	4	US-08-469-260A-576	Sequence 576, App
61	34	12.7	10	4	US-08-488-446-576	Sequence 576, App
62	34	12.7	10	4	US-08-467-344A-576	Sequence 576, App
63	34	12.7	10	4	US-08-424-550B-576	Sequence 576, App
64	34	12.7	19	4	US-09-050-861B-16	Sequence 16, Appl
65	34	12.7	19	4	US-09-135-238B-16	Sequence 16, Appl
66	34	12.7	21	1	US-08-295-411-6	Sequence 6, Appli
67	34	12.7	21	2	US-08-955-471-6	Sequence 6, Appli
68	34	12.7	21	5	PCT-US92-10242-6	Sequence 6, Appli
69	34	12.7	29	1	US-08-119-169A-5	Sequence 5, Appli
70	34	12.7	32	1	US-08-137-117D-130	Sequence 130, App
71	34	12.7	32	1	US-08-137-117D-132	Sequence 132, App
72	34	12.7	32	2	US-08-436-717-130	Sequence 130, App
73	34	12.7	32	2	US-08-436-717-132	Sequence 132, App
74	34	12.7	32	4	US-09-647-468-116	Sequence 116, App
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77	34	12.7	39	4	US-09-270-767-57067	Sequence 57067, A
78	34	12.7	41	1	US-08-597-495B-28	Sequence 28, Appl
79	34	12.7	41	2	US-08-117-952-794	Sequence 794, App
80	34	12.7	41	2	US-08-640-847C-28	Sequence 28, Appl
81	34	12.7	41	3	US-09-068-051A-28	Sequence 28, Appl
82	34	12.7	41	3	US-09-306-446C-3	Sequence 3, Appli
83	34	12.7	43	4	US-08-454-899G-109	Sequence 109, App
84	34	12.7	46	2	US-08-613-235-1	Sequence 1, Appli
85	33.5	12.5	47	4	US-09-471-276-1388	Sequence 1388, Ap
86	33	12.3	11	1	US-08-445-745-67	Sequence 67, Appl
87	33	12.3	11	3	US-08-456-466-44	Sequence 44, Appl
88	33	12.3	11	4	US-08-445-638-67	Sequence 67, Appl
89	33	12.3	11	4	US-09-951-902-8	Sequence 8, Appli
90	33	12.3	12	4	US-09-383-062-29	Sequence 29, Appl
91	33	12.3	15	1	US-07-859-291C-31	Sequence 31, Appl
92	33	12.3	15	1	US-08-664-449-33	Sequence 33, Appl
93	33	12.3	15	4	US-09-142-524D-98	Sequence 98, Appl
94	33	12.3	20	1	US-08-787-547-23	Sequence 23, Appl
95	33	12.3	20	3	US-08-523-373-1	Sequence 1, Appli
96	33	12.3	24	1	US-08-657-192-10	Sequence 10, Appl
97	33	12.3	24	1	US-08-484-635-108	Sequence 108, App
98	33	12.3	24	2	US-08-484-631-108	Sequence 108, App
99	33	12.3	24	2	US-08-827-570-108	Sequence 108, App
100	33	12.3	26	1	US-08-352-179-21	Sequence 21, Appl

ALIGNMENTS

```
RESULT 1
US-09-345-468-7
; Sequence 7, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva1, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-345-468-7

Query Match      100.0%; Score 268; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.8e-31;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||
Db      1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47

RESULT 2
US-09-414-453A-7
; Sequence 7, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva1, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-414-453A-7

Query Match      100.0%; Score 268; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.8e-31;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47
      |||
Db      1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47

RESULT 3
US-09-345-468-23
; Sequence 23, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva1, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-345-468-23

Query Match      100.0%; Score 268; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.8e-31;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47
      |||
Db      1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47
```

```
; APPLICANT: Villeva1, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-345-468-23

Query Match      82.1%; Score 220; DB 3; Length 47;
Best Local Similarity 78.7%; Pred. No. 2.8e-24;
Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47
      |||
Db      1 CQSPYSFDEFVLVYKEGDTGPKYRPEKWKYRANFPFIITVTAHSGTYRC 47

RESULT 4
US-09-414-453A-23
; Sequence 23, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villeva1, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-414-453A-23

Query Match      82.1%; Score 220; DB 3; Length 47;
Best Local Similarity 78.7%; Pred. No. 2.8e-24;
Matches 37; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 CQTRYGFDQFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47
      |||
Db      1 CQSPYSFDEFVLVYKEGDTGPKYRPEKWKYRANFPFIITVTAHSGTYRC 47

RESULT 5
US-08-726-306A-119
; Sequence 119, Application US/08726306A
; Patent No. 5958684
; GENERAL INFORMATION:
; APPLICANT: van Leeuwen, Frederik Willem
; APPLICANT: Burbach, Johannes Peter Henri
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1 Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
```


COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 119:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-726-306A-119

Query Match 17.4%; Score 46.5; DB 2; Length 38;
Best Local Similarity 58.8%; Pred. No. 14;
Matches 10; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 13 YKEG-DPAPYKNPERWY 28
: || ||||| |||||
Db 3 HPEGVDPAPGPASERWY 19

RESULT 6
US-08-726-306A-122
Sequence 122, Application US/08726306A
Patent No. 5958684
GENERAL INFORMATION:
APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380

REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-726-306A-122

Query Match 17.4%; Score 46.5; DB 2; Length 38;
Best Local Similarity 58.8%; Pred. No. 14;
Matches 10; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

QY 13 YKEG-DPAPYKNPERWY 28
: || ||||| |||||
Db 3 HPEGVDPAPGPASERWY 19

RESULT 7
US-08-476-866-23
Sequence 23, Application US/08476866
Patent No. 5994339
GENERAL INFORMATION:
APPLICANT: CRAPO, JAMES D.
APPLICANT: FRIDOVICH, IRWIN
APPLICANT: OURY, TIM
APPLICANT: DAY, BRIAN J.
APPLICANT: FOLZ, RODNEY J.
APPLICANT: FREEMAN, BRUCE A.
TITLE OF INVENTION: SUPEROXIDE DISMUTASE AND MIMETICS THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,866
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/322,766
FILING DATE: 13-OCT-1994
APPLICATION NUMBER: US 08/136,207
FILING DATE: 15-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-74
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-476-866-23

```
Query Match      17.2%; Score 46; DB 2; Length 42;
Best Local Similarity 48.0%; Pred. No. 19;
Matches 12; Conservative 1; Mismatches 12; Indels 0; Gaps 0;

Qy      18 PAPYKNPWRWYRASFPILITVTAHNS 42
Db      11 PAPSTPSPWRASRPSRTAPAAP 35

RESULT 8
US-08-254-095-1
; Sequence 1, Application US/08254095
; Patent No. 5804189
; GENERAL INFORMATION:
; APPLICANT: Goyert, Sanna S.
; TITLE OF INVENTION: A No. 5804189el Thgerapy for Treating Symptoms
; TITLE OF INVENTION: of Sepsis Using A Soluble Form of Recombinant CD14
; TITLE OF INVENTION: Myelomonocytic Antigen
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenyon & Kenyon
; STREET: One Broadway
; CITY: New York
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/254,095
; FILING DATE: 06-JUN-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/863,913
; FILING DATE: 06-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Sinder, Stuart J
; REFERENCE/DOCKET NUMBER: 52492/1002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 425-7200
; TELEFAX: (212) 425-5288
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-254-095-1

Query Match      16.4%; Score 44; DB 1; Length 26;
Best Local Similarity 21.7%; Pred. No. 20;
Matches 5; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy      25 ERWYRASFPILITVTAHSGTYRC 47
Db      4 QQWLKPKGLKVLISIAQAHSINPSC 26

RESULT 9
US-09-132-769-17
; Sequence 17, Application US/09132769A
; Patent No. 6525023
; GENERAL INFORMATION:
; APPLICANT: Motoo Yamasaki
; APPLICANT: Kenji Shibata
```

```
; APPLICANT: No. 6525023uo Hanai
; APPLICANT: Akiko Furuya
; APPLICANT: Kaoru Miyamoto
; TITLE OF INVENTION: NOVEL VASCULAR SMOOTH MUSCLE CELL GROWTH FACTOR
; FILE REFERENCE: 11078
; CURRENT APPLICATION NUMBER: US/09/132,769A
; CURRENT FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: HEI9-218491
; EARLIER FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 30
; TYPE: PRT
; ORGANISM: BOVINE
US-09-132-769-17

Query Match      16.4%; Score 44; DB 4; Length 30;
Best Local Similarity 53.3%; Pred. No. 24;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy      4 RYGFDPQFALYKEGDP 18
Db      16 REGYTEFSLRVEGDP 30

RESULT 10
US-09-043-731-13
; Sequence 13, Application US/09043731A
; Patent No. 6344203
; GENERAL INFORMATION:
; APPLICANT: The Austin Research Institute
; TITLE OF INVENTION: Mimicking Peptides in Cancer Therapy
; FILE REFERENCE: CALA-200
; CURRENT APPLICATION NUMBER: US/09/043,731A
; CURRENT FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: single
; OTHER INFORMATION: stranded linear peptide
US-09-043-731-13

Query Match      16.0%; Score 43; DB 3; Length 28;
Best Local Similarity 40.0%; Pred. No. 31;
Matches 8; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy      28 YRASFPILITVTAHSGTYRC 47
Db      5 YSSNFSIPKANHSHSGDYIC 24

RESULT 11
US-09-345-468-22
; Sequence 22, Application US/09345468
; Patent No. 6245527
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevall, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/345,468
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 41
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```

; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-345-468-22

Query Match 16.0%; Score 43; DB 3; Length 41;
Best Local Similarity 29.2%; Pred. No. 50;
Matches 14; Conservative 7; Mismatches 19; Indels 8; Gaps 2;

QY 1 CQTRYGDFQFALYKEGDPAPYKNPERWYRASFPPII-TVTAHSGTYRC 47
Db 1 CQGPDPVDLYRLEK-----LKPEKYEDQDFLFIPTMERSNAGRYRC 41

RESULT 12
US-09-414-453A-22
; Sequence 22, Application US/09414453A
; Patent No. 6383779
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Villevial, J.
; APPLICANT: Jandrot-Perrus, M.
; APPLICANT: Vainchenker, W.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-147
; CURRENT APPLICATION NUMBER: US/09/414,453A
; CURRENT FILING DATE: 1999-10-07
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 41
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-414-453A-22

Query Match 16.0%; Score 43; DB 3; Length 41;
Best Local Similarity 29.2%; Pred. No. 50;
Matches 14; Conservative 7; Mismatches 19; Indels 8; Gaps 2;

QY 1 CQTRYGDFQFALYKEGDPAPYKNPERWYRASFPPII-TVTAHSGTYRC 47
Db 1 CQGPDPVDLYRLEK-----LKPEKYEDQDFLFIPTMERSNAGRYRC 41

RESULT 13
US-08-332-562A-22
; Sequence 22, Application US/08332562A
; Patent No. 5985599
; GENERAL INFORMATION:
; APPLICANT: MCKENZIE, Ian F.C.
; APPLICANT: HOGARTH, Mark P.
; APPLICANT: HIBBS, Margaret L.
; APPLICANT: SCOTT, Bernadette M.
; APPLICANT: BONADONNA, Lisa
; APPLICANT: HULETT, Mark D.
; TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,562A
; FILING DATE: 31-OCT-1994

```

1	EARLIER APPLICATION NUMBER: 60/048,901
2	EARLIER FILING DATE: 1997-06-06
3	EARLIER APPLICATION NUMBER: 60/048,892
4	EARLIER FILING DATE: 1997-06-06
5	EARLIER APPLICATION NUMBER: 60/048,915
6	EARLIER FILING DATE: 1997-06-06
7	EARLIER APPLICATION NUMBER: 60/049,019
8	EARLIER FILING DATE: 1997-06-06
9	EARLIER APPLICATION NUMBER: 60/048,970
10	EARLIER FILING DATE: 1997-06-06
11	EARLIER APPLICATION NUMBER: 60/048,972
12	EARLIER FILING DATE: 1997-06-06
13	EARLIER APPLICATION NUMBER: 60/048,916
14	EARLIER FILING DATE: 1997-06-06
15	EARLIER APPLICATION NUMBER: 60/049,373
16	EARLIER FILING DATE: 1997-06-06
17	EARLIER APPLICATION NUMBER: 60/048,875
18	EARLIER FILING DATE: 1997-06-06
19	EARLIER APPLICATION NUMBER: 60/049,374
20	EARLIER FILING DATE: 1997-06-06
21	EARLIER APPLICATION NUMBER: 60/048,917
22	EARLIER FILING DATE: 1997-06-06
23	EARLIER APPLICATION NUMBER: 60/048,949
24	EARLIER FILING DATE: 1997-06-06
25	EARLIER APPLICATION NUMBER: 60/048,974
26	EARLIER FILING DATE: 1997-06-06
27	EARLIER APPLICATION NUMBER: 60/048,883
28	EARLIER FILING DATE: 1997-06-06
29	EARLIER APPLICATION NUMBER: 60/048,897
30	EARLIER FILING DATE: 1997-06-06
31	EARLIER APPLICATION NUMBER: 60/048,898
32	EARLIER FILING DATE: 1997-06-06
33	EARLIER APPLICATION NUMBER: 60/048,962
34	EARLIER FILING DATE: 1997-06-06
35	EARLIER APPLICATION NUMBER: 60/048,963
36	EARLIER FILING DATE: 1997-06-06
37	EARLIER APPLICATION NUMBER: 60/048,877
38	EARLIER FILING DATE: 1997-06-06
39	EARLIER APPLICATION NUMBER: 60/048,878
40	EARLIER FILING DATE: 1997-06-06
41	EARLIER APPLICATION NUMBER: 60/070,923
42	EARLIER FILING DATE: 1997-12-18
43	EARLIER APPLICATION NUMBER: 60/092,921
44	EARLIER FILING DATE: 1998-07-15
45	EARLIER APPLICATION NUMBER: 60/094,657
46	EARLIER FILING DATE: 1998-07-30
47	NUMBER OF SEQ ID NOS: 1227
48	SOFTWARE: PatentIn Ver. 2.0
49	SEQ ID NO 646
50	LENGTH: 30
51	TYPE: PRT
52	ORGANISM: Homo sapiens
53	JS-09-205-258-646

Query Match	15.7%	Score 42;	DB 4;	Length 30;
Best Local Similarity	34.3%	Pred. No. 47;		
Matches	12: Conservative	4: Mismatches	9: Indels	10: Gaps

Qy	1	CQT-RYGFDQFALYKEGDPAPYKNPERWYRASEPI	34
		: :	
Dp	4	CLTVRWAFESLOV-----PQWRPERW-ASEPI	29

RESULT 15
US-09-443-780C-57
; Sequence 57, Application US/09443780C
; Patent No. 6699973
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J
; APPLICANT: Seveso, Michela
; TITLE OF INVENTION: Antibodies To Pe
; FILE REFERENCE: E1067/20037
; CURRENT APPLICATION NUMBER: US/09/443

```

; CURRENT FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 60/109,036
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PAX45 39 mer fragment L-form
US-09-443-780C-57

```

Query Match	15.3%	Score 41;	DB 4;	Length 39;
Best Local Similarity	38.5%;	Pred. No. 91;		
Matches 10;	Conservative	4;	Mismatches 10;	Indels 2;
			Gaps 1;	

QY 5 YGFDQFALYKEGDPAPYKNPERWYRA 30
: : : : :
db 8 HGLERHAL--DGTGTPLYAMPGRWLRA 31

```

RESULT 16
US-09-079-723-41
; Sequence 41, Application US/09079723
; Patent No. 6703362
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Singleton, Judith
; APPLICANT: Patterson, Catherine A.
; APPLICANT: Cagney, Gerard M.
; APPLICANT: Belinka, Benjamin A.
; APPLICANT: Carter, John M.
; TITLE OF INVENTION: RANDOM PEPTIDES THAT BIND TO GASTRO-
; TITLE OF INVENTION: INTESTINAL TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,723
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-219
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 39 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
;
US-09-079-723-41
Query Match 15.3%; Score 41; DB 4; Length 39;
Best Local Similarity 38.5%; Pred. No. 91;

```

```

; APPLICANT: Seveso, Michela
; TITLE OF INVENTION: Antibodies To Peptides That Target GIT Receptors And Related Meth
; FILE REFERENCE: E1067/20037
; CURRENT APPLICATION NUMBER: US/09/443,780C

```

Matches 10; Conservative 4; Mismatches 10; Indels 2; Gaps 1;
Qy 5 YGFDQFALYKEGDPAPYKNPERWYRA 30
Db 8 HGLERHAL--DGTGPLYAMPGRWIRA 31

RESULT 17
US-08-726-306A-125
; Sequence 125, Application US/08726306A
; Patent No. 5958684
; GENERAL INFORMATION:
; APPLICANT: van Leeuwen, Frederik Willem
; APPLICANT: Burbach, Johannes Peter Henri
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
; NUMBER OF SEQUENCES: 189
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1 Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,306A
; FILING DATE: 02-Oct-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 95/20080.4
; FILING DATE: 02-Oct-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/009,832
; FILING DATE: 01-Jan-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-726-306A-125

Query Match 15.1%; Score 40.5; DB 2; Length 26;
Best Local Similarity 56.2%; Pred. No. 65;
Matches 9; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
Qy 13 YKEG-DPAPYKNPERW 27
Db 3 HPEGVDPAPEGW 18

RESULT 18
US-08-332-562A-21
; Sequence 21, Application US/08332562A
; Patent No. 5985599
; GENERAL INFORMATION:
; APPLICANT: MCKENZIE, Ian F.C.
; APPLICANT: HOGARTH, Mark P.
; APPLICANT: HIBBS, Margaret L.
; APPLICANT: SCOTT, Bernadette M.
; APPLICANT: BONADONNA, Lisa

; APPLICANT: HULETT, Mark D.
; TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,562A
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/896,457
; FILING DATE: 27-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 54270/119/GRHA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-332-562A-21

Query Match 15.1%; Score 40.5; DB 2; Length 43;
Best Local Similarity 27.9%; Pred. No. 1.2e+02;
Matches 12; Conservative 5; Mismatches 15; Indels 11; Gaps 2;
Qy 15 EGDPAKYKNPERWY-----RASFPITVTAHSGTYRC 47
Db 2 EGTNPGNSSTQWFHNGRSIRSQVQASY-TFKATVNDSGEYRC 43

RESULT 19
US-10-027-038-5
; Sequence 5, Application US/10027038
; Patent No. 6822073
; GENERAL INFORMATION:
; APPLICANT: Quirk, S.
; TITLE OF INVENTION: Modular peptide-based reagent
; FILE REFERENCE: 1443.026US1
; CURRENT APPLICATION NUMBER: US/10/027,038
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide backbone.
US-10-027-038-5

Query Match 14.9%; Score 40; DB 4; Length 36;
Best Local Similarity 34.6%; Pred. No. 1.1e+02;
Matches 9; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
Qy 16 GDPAPYKNPERWYRASFPITVTAH 41

Db 9 GDPAPVEDLIRFYDNLQQLNVVTRH 34

RESULT 20

US-08-251-472-10
; Sequence 10, Application US/08251472
; Patent No. 5871746
; GENERAL INFORMATION:
; APPLICANT: BOUTILLON, CHRISTOPHE; MARTINON,
; APPLICANT: FREDERIC; GRAS-MASSE, HELENE;
; APPLICANT: GOMARD, ELISABETH; SERGHERAERT,
; APPLICANT: CHRISTIAN; MAGNE, REMY; TARTAR,
; APPLICANT: ANDRE; LEVY, JEAN-PAUL

; TITLE OF INVENTION: CYTOTOXIC T LYMPHOCYTE
; TITLE OF INVENTION: -INDUCING LIPOPEPTIDES AND USE AS VACCINES

; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016

; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/251,472
; FILING DATE: 31-MAY-1994
; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:
; NAME: MUSERLIAN, CHARLES A
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 102.1511

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: SIV
; FEATURE:
; LOCATION: GAG 246-281

US-08-251-472-10

Query Match 14.6%; Score 39; DB 2; Length 36;
Best Local Similarity 37.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 12 LYKEGDPAPYKNPERW 27

:|:::| | | |

Db 5 MYRQQNPPIPVGNIYRW 20

RESULT 21

US-09-248-082-10
; Sequence 10, Application US/09248082
; Patent No. 6015564
; GENERAL INFORMATION:
; APPLICANT: BOUTILLON, CHRISTOPHE; MARTINON,
; APPLICANT: FREDERIC; GRAS-MASSE, HELENE;
; APPLICANT: GOMARD, ELISABETH; SERGHERAERT,
; APPLICANT: CHRISTIAN; MAGNE, REMY; TARTAR,
; APPLICANT: ANDRE; LEVY, JEAN-PAUL

; TITLE OF INVENTION: CYTOTOXIC T LYMPHOCYTE

; TITLE OF INVENTION: -INDUCING LIPOPEPTIDES AND USE AS VACCINES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BIERMAN & MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016

; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/248,082
; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/251,472
; FILING DATE: 31-MAY-1994

; ATTORNEY/AGENT INFORMATION:
; NAME: MUSERLIAN, CHARLES A
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 102.1511

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002

; INFORMATION FOR SEQ ID NO: 10:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 36

; TYPE: amino acid

; STRANDEDNESS: unknown

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FRAGMENT TYPE: internal

; ORIGINAL SOURCE:

; ORGANISM: SIV

; FEATURE:

; LOCATION: GAG 246-281

US-09-248-082-10

Query Match 14.6%; Score 39; DB 3; Length 36;
Best Local Similarity 37.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 12 LYKEGDPAPYKNPERW 27

:|:::| | | |

Db 5 MYRQQNPPIPVGNIYRW 20

RESULT 22

US-10-027-038-14
; Sequence 14, Application US/10027038
; Patent No. 6822073
; GENERAL INFORMATION:
; APPLICANT: Quirk, S.
; TITLE OF INVENTION: Modular peptide-based reagent
; FILE REFERENCE: 1443.026US1
; CURRENT APPLICATION NUMBER: US/10/027,038
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide backbone.

US-10-027-038-14

Query Match 14.4%; Score 38.5; DB 4; Length 35;
Best Local Similarity 34.4%; Pred. No. 1.8e+02;

Matches 11; Conservative 2; Mismatches 6; Indels 13; Gaps 2;

QY 16 GDPAP-----YKNPERWYRASFPPIITVTAA 40
||| | | : | | |
Db 9 GDPGPVEDLIRFYDNLQWLNC-----VTAA 34

RESULT 23

US-10-027-038-11
; Sequence 11, Application US/10027038
; Patent No. 6822073
; GENERAL INFORMATION:
; APPLICANT: Quirk, S.
; TITLE OF INVENTION: Modular peptide-based reagent
; FILE REFERENCE: 1443.026US1
; CURRENT APPLICATION NUMBER: US/10/027,038
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A peptide backbone.
US-10-027-038-11

Query Match 14.4%; Score 38.5; DB 4; Length 36;
Best Local Similarity 34.4%; Pred. No. 1.9e+02;
Matches 11; Conservative 2; Mismatches 6; Indels 13; Gaps 2;

QY 16 GDPAP-----YKNPERWYRASFPPIITVTAA 40
||| | | : | | |
Db 10 GDPGPVEDLIRFYDNLQWLNC-----VTAA 35

RESULT 24

US-09-763-331-7
; Sequence 7, Application US/09763331
; Patent No. 6825335
; GENERAL INFORMATION:
; APPLICANT: Martin, Charles E.
; APPLICANT: Mitchell, Andrew
; TITLE OF INVENTION: Synthetic Fatty Acid Desaturase Gene for
; TITLE OF INVENTION: Expression in Plants
; FILE REFERENCE: 97-0081 PCT
; CURRENT APPLICATION NUMBER: US/09/763,331
; CURRENT FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: US 60/097,586
; PRIOR FILING DATE: 1998-08-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-763-331-7

Query Match 14.2%; Score 38; DB 4; Length 33;
Best Local Similarity 30.8%; Pred. No. 2e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 8; Gaps 1;

QY 11 ALYKEGDPAPYKNPER-----WY 28
|:|:| | | : | |
Db 4 AMYREAKECIYVEPDREGDKKGVWY 29

RESULT 25

US-08-332-562A-27
; Sequence 27, Application US/08332562A
; Patent No. 5985599
; GENERAL INFORMATION:
; APPLICANT: MCKENZIE, Ian F.C.

; APPLICANT: HOGARTH, Mark P.
; APPLICANT: HIBBS, Margaret L.
; APPLICANT: SCOTT, Bernadette M.
; APPLICANT: BONADONNA, Lisa
; APPLICANT: HULETT, Mark D.
; TITLE OF INVENTION: PC RECEPTOR FOR IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 136
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,562A
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/896,457
; FILING DATE: 27-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 54270/119/GRHA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-332-562A-27

Query Match 14.2%; Score 38; DB 2; Length 45;
Best Local Similarity 41.2%; Pred. No. 2.9e+02;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 31 SFPITVTAAHSGTYRC 47
:|:| | | | : | | |
Db 29 TFSIPQANHSHSGDYHC 45

Search completed: October 29, 2005, 04:28:36
Job time : 44 secs

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OM protein - protein search, using sw model

Run on: October 29, 2005, 04:25:07 ; Search time 165 Seconds
(without alignments)
119.079 Million cell updates/sec

Title: US-09-503-387-3_COPY_134_180
Perfect score: 268
Sequence: 1 CQTRYGDFQFALYKEGDPAP.....YRASFPITVTAHSGTYRC 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 535388

Minimum DB seq length: 0
Maximum DB seq length: 48

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA:*
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22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	268	100.0	47	9	US-09-832-312-7
2	268	100.0	47	11	US-09-829-495-7
3	268	100.0	47	16	US-10-850-034-7
4	220	82.1	47	9	US-09-832-312-23
5	220	82.1	47	11	US-09-829-495-23
6	220	82.1	47	16	US-10-850-034-23
7	47	17.5	45	15	US-10-424-599-152673
8	46.5	17.4	26	15	US-10-403-847-143
9	46.5	17.4	34	14	US-10-040-862-9616
10	46.5	17.4	34	15	US-10-057-475B-9616
11	46.5	17.4	34	15	US-10-154-884B-9616
					Sequence 7, Appli
					Sequence 7, Appli
					Sequence 23, Appl
					Sequence 23, Appl
					Sequence 143, App
					Sequence 9616, Ap
					Sequence 9616, Ap
					Sequence 9616, Ap

12	46.5	17.4	34	16	US-10-764-324-9616	Sequence 9616, Ap
13	46	17.2	32	16	US-10-425-115-325445	Sequence 325445,
14	45.5	17.0	44	14	US-10-321-857-60	Sequence 60, Appl
15	45.5	17.0	44	14	US-10-318-675-60	Sequence 60, Appl
16	45	16.8	24	17	US-10-477-525-15	Sequence 15, Appl
17	45	16.8	30	14	US-10-040-862-10445	Sequence 10445, A
18	45	16.8	30	15	US-10-057-475B-10445	Sequence 10445, A
19	45	16.8	30	15	US-10-154-884B-10445	Sequence 10445, A
20	45	16.8	30	16	US-10-764-324-10445	Sequence 10445, A
21	45	16.8	41	15	US-10-154-884B-11154	Sequence 11154, A
22	45	16.8	43	15	US-10-424-599-179261	Sequence 179261,
23	44.5	16.6	45	9	US-09-764-869-997	Sequence 997, App
24	44.5	16.6	45	14	US-10-091-504-997	Sequence 997, App
25	44.5	16.6	45	15	US-10-227-577-997	Sequence 997, App
26	44.5	16.6	45	16	US-10-425-115-195108	Sequence 195108,
27	44	16.4	34	15	US-10-424-599-173732	Sequence 173732,
28	44	16.4	42	9	US-09-731-449-21	Sequence 21, Appl
29	44	16.4	42	14	US-10-254-426-21	Sequence 21, Appl
30	44	16.4	46	16	US-10-425-115-348493	Sequence 348493,
31	44	16.4	47	9	US-09-731-449-22	Sequence 22, Appl
32	44	16.4	47	9	US-09-731-449-23	Sequence 23, Appl
33	44	16.4	47	13	US-10-105-934-17	Sequence 17, Appl
34	44	16.4	47	14	US-10-254-426-22	Sequence 22, Appl
35	44	16.4	47	14	US-10-254-426-23	Sequence 23, Appl
36	44	16.4	47	17	US-10-895-676-17	Sequence 17, Appl
37	43	16.0	13	15	US-10-462-452-374	Sequence 374, App
38	43	16.0	13	15	US-10-462-452-390	Sequence 390, App
39	43	16.0	13	15	US-10-601-953-502	Sequence 502, App
40	43	16.0	13	15	US-10-601-953-518	Sequence 518, App
41	43	16.0	13	16	US-10-322-266-375	Sequence 375, App
42	43	16.0	13	16	US-10-322-266-376	Sequence 376, App
43	43	16.0	13	16	US-10-322-266-391	Sequence 391, App
44	43	16.0	14	15	US-10-462-452-375	Sequence 375, App
45	43	16.0	14	15	US-10-462-452-391	Sequence 391, App
46	43	16.0	14	15	US-10-601-953-503	Sequence 503, App
47	43	16.0	14	15	US-10-601-953-519	Sequence 519, App
48	43	16.0	14	16	US-10-322-266-392	Sequence 392, App
49	43	16.0	17	15	US-10-462-452-369	Sequence 369, App
50	43	16.0	17	15	US-10-462-452-385	Sequence 385, App
51	43	16.0	17	15	US-10-601-953-497	Sequence 497, App
52	43	16.0	17	15	US-10-601-953-513	Sequence 513, App
53	43	16.0	17	16	US-10-322-266-370	Sequence 370, App
54	43	16.0	17	16	US-10-322-266-386	Sequence 386, App
55	43	16.0	19	15	US-10-462-452-370	Sequence 370, App
56	43	16.0	19	15	US-10-462-452-386	Sequence 386, App
57	43	16.0	19	15	US-10-601-953-498	Sequence 498, App
58	43	16.0	19	15	US-10-601-953-514	Sequence 514, App
59	43	16.0	19	16	US-10-322-266-371	Sequence 371, App
60	43	16.0	19	16	US-10-322-266-387	Sequence 387, App
61	43	16.0	30	15	US-10-057-475B-10834	Sequence 10834, A
62	43	16.0	30	15	US-10-154-884B-10834	Sequence 10834, A
63	43	16.0	39	15	US-10-424-599-255712	Sequence 255712,
64	43	16.0	41	9	US-09-832-312-22	Sequence 22, Appl
65	43	16.0	41	11	US-09-829-495-22	Sequence 22, Appl
66	43	16.0	41	16	US-10-850-034-22	Sequence 22, Appl
67	42.5	15.9	21	15	US-10-312-829-17	Sequence 17, Appl
68	42	15.7	12	15	US-10-462-452-373	Sequence 373, App
69	42	15.7	12	15	US-10-462-452-389	Sequence 389, App
70	42	15.7	12	15	US-10-601-953-501	Sequence 501, App
71	42	15.7	12	15	US-10-601-953-517	Sequence 517, App
72	42	15.7	12	15	US-10-322-266-374	Sequence 374, App
73	42	15.7	12	16	US-10-322-266-390	Sequence 390, App
74	42	15.7	15	15	US-10-462-452-368	Sequence 368, App
75	42	15.7	15	15	US-10-462-452-384	Sequence 384, App
76	42	15.7	15	15	US-10-601-953-496	Sequence 496, App
77	42	15.7	15	15	US-10-601-953-512	Sequence 512, App
78	42	15.7	15	16	US-10-322-266-369	Sequence 369, App
79	42	15.7	15	16	US-10-322-266-385	Sequence 385, App
80	42	15.7	30	10	US-09-933-767-646	Sequence 646, App
81	42	15.7	30	14	US-10-004-860-646	Sequence 646, App
82	42	15.7	30	14	US-10-023-282-646	Sequence 646, App
83	42	15.7	47	16	US-10-425-115-282892	Sequence 282892,
84	41	15.3	16	15	US-10-403-847-111	Sequence 111, App

85	41	15.3	26	14	US-10-231-417-491	Sequence 491, App
86	41	15.3	32	10	US-09-791-551-34	Sequence 34, Appl
87	41	15.3	39	16	US-10-751-699-57	Sequence 57, Appl
88	41	15.3	45	15	US-10-424-599-256207	Sequence 256207,
89	41	15.3	46	10	US-09-874-141-33	Sequence 33, Appl
90	41	15.3	46	10	US-09-874-141-36	Sequence 36, Appl
91	40.5	15.1	35	9	US-09-864-761-40395	Sequence 40395, A
92	40.5	15.1	45	14	US-10-097-065-607	Sequence 607, App
93	40.5	15.1	45	15	US-10-372-876-607	Sequence 607, App
94	40.5	15.1	48	16	US-10-437-963-178387	Sequence 178387,
95	40.5	15.1	48	16	US-10-767-701-47178	Sequence 47178, A
96	40	14.9	13	15	US-10-601-953-438	Sequence 438, App
97	40	14.9	13	15	US-10-601-953-454	Sequence 454, App
98	40	14.9	14	15	US-10-601-953-439	Sequence 439, App
99	40	14.9	14	15	US-10-601-953-455	Sequence 455, App
100	40	14.9	16	15	US-10-403-847-107	Sequence 107, App

ALIGNMENTS

```

RESULT 1
US-09-832-312-7
; Sequence 7, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-7

```

```

Query Match      100.0%; Score 268; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.1e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CQRYGDFQFALYKEGPAPYKNPERWYRASFPPIITVTAHSGTYRC 47

RESULT 2
US-09-829-495-7
; Sequence 7, Application US/09829495
; Publication No. US20040001826A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/829,495
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30

```

; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-829-495-7

```

Query Match 100.0%; Score 268; DB 11; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.1e-26;
Matches 47; Conservative 0; Mismatches 0; Indels

QY 1 CQRYGTDQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTVRC 47
|||
db 1 CQRYGTDQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTVRC 47

```

RESULT 3
US-10-850-034-7
; Sequence 7, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ
; APPLICANT: Villevall J
; APPLICANT: Jandrot-Perrus M
; APPLICANT: Vainchenker W
; APPLICANT: Gill DS
; APPLICANT: Qian MD
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/10/850,034
; CURRENT FILING DATE: 2004-05-20
; PRIOR APPLICATION NUMBER: US/09/829,495
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-850-034-7

```

Query Match	100.0%;	Score 268;	DB 16;	Length 47;
Best Local Similarity	100.0%;	Pred. No. 1.1e-26;		
Matches 47;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 CQTRYGFDQFALYKEGDPAPYKKNPERWYRASFPILITVTTAAHSGTVRC 47

Db 1 CQTRYGFDQFALYKEGDPAPYKKNPERWYRASFPILITVTTAAHSGTVRC 47

RESULT 4
US-09-832-312-23
; Sequence 23, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234

RESULT 6
US-10-850-034-23
; Sequence 23, Application US/10850034
; Publication No. US20040253236A1
; GENERAL INFORMATION:
; APPLICANT: Busfield SJ

RESULT 8

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US-10-403-847-143
; Sequence 143, Application US/10403847
; Publication No. US20040030098A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL TWO SPLICE VARIANTS OF A HUMAN
; FILE REFERENCE: D0228 NP
; CURRENT APPLICATION NUMBER: US/10/403,847
; CURRENT FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: U.S. 60/368,671
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: U.S. 60/371,420
; PRIOR FILING DATE: 2002-04-10
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 143
; LENGTH: 26
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-847-143

Query Match      17.4%; Score 46.5; DB 15; Length 26;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY      30 ASFPITVTAAHSGTYRC 47
      ||| :::||| |||
Db      6 ASFN-LSLTAHSGNYSC 22

RESULT 9
US-10-040-862-9616
; Sequence 9616, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9616
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-9616

Query Match      17.4%; Score 46.5; DB 15; Length 34;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY      30 ASFPITVTAAHSGTYRC 47
      ||| :::||| |||
Db      12 ASFN-LSLTAHSGNYSC 28
```

```
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9616
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-9616

Query Match      17.4%; Score 46.5; DB 14; Length 34;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY      30 ASFPITVTAAHSGTYRC 47
      ||| :::||| |||
Db      12 ASFN-LSLTAHSGNYSC 28

RESULT 10
US-10-057-475B-9616
; Sequence 9616, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9616
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-475B-9616

Query Match      17.4%; Score 46.5; DB 15; Length 34;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY      30 ASFPITVTAAHSGTYRC 47
      ||| :::||| |||
Db      12 ASFN-LSLTAHSGNYSC 28
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```
RESULT 11
US-10-154-884B-9616
; Sequence 9616, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9616
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-154-884B-9616

Query Match      17.4%; Score 46.5; DB 15; Length 34;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY      30 ASFPITVTAAHSGTYRC 47
      ||| :||| ||| |||
Db      12 ASFN-LSLTAHSGNYSC 28

RESULT 12
US-10-764-324-9616
; Sequence 9616, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/764,324
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/10/040,862
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479

Query Match      17.4%; Score 46.5; DB 15; Length 34;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY      30 ASFPITVTAAHSGTYRC 47
      ||| :||| ||| |||
Db      12 ASFN-LSLTAHSGNYSC 28

RESULT 13
US-10-425-115-325445
; Sequence 325445, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 325445
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(32)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_59877C.1.pep
US-10-425-115-325445

Query Match      17.2%; Score 46; DB 16; Length 32;
Best Local Similarity 44.4%; Pred. No. 1.8e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      18 PAPYKNPERWYRASFPPII 35
      ||| :||| ||| |||
Db      7 PPPAESPPYRGRLPPII 24

RESULT 14
US-10-321-857-60
; Sequence 60, Application US/10321857
; Publication No. US20030180816A1
```

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; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9616
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-324-9616

Query Match      17.4%; Score 46.5; DB 16; Length 34;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 10; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY      30 ASFPITVTAAHSGTYRC 47
      ||| :||| ||| |||
Db      12 ASFN-LSLTAHSGNYSC 28

RESULT 13
US-10-425-115-325445
; Sequence 325445, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 325445
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(32)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_59877C.1.pep
US-10-425-115-325445

Query Match      17.2%; Score 46; DB 16; Length 32;
Best Local Similarity 44.4%; Pred. No. 1.8e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY      18 PAPYKNPERWYRASFPPII 35
      ||| :||| ||| |||
Db      7 PPPAESPPYRGRLPPII 24

RESULT 14
US-10-321-857-60
; Sequence 60, Application US/10321857
; Publication No. US20030180816A1
```

; GENERAL INFORMATION:
; APPLICANT: Applied NanoSystems B.V.
; TITLE OF INVENTION: A method to provide bacterial ghosts with antigens
; FILE REFERENCE: 2183-5547US
; CURRENT APPLICATION NUMBER: US/10/321,857
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/NL02/00383
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 01202239.8
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Pseudomonas putida
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(44)
; OTHER INFORMATION: Acma cell wall binding domain homologue
; US-10-321-857-60

Query Match 17.0%; Score 45.5; DB 14; Length 44;
Best Local Similarity 52.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 1; Mismatches 1; Indels 9; Gaps 2;

QY 4 RYGFQDPALYKE-----GDPAPY 21
Db 15 RYGWD----YKELAAARNGIPAPY 33

RESULT 15
US-10-318-675-60
; Sequence 60, Application US/10318675
; Publication No. US20030186851A1
; GENERAL INFORMATION:
; APPLICANT: Applied NanoSystems B.V.
; TITLE OF INVENTION: Bacterial ghosts provided with antigens
; FILE REFERENCE: 2183-5546US
; CURRENT APPLICATION NUMBER: US/10/318,675
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/NL02/00383
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: 01202239.8
; PRIOR FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Pseudomonas putida
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)..(44)
; OTHER INFORMATION: Acma cell wall binding domain homologue
; US-10-318-675-60

Query Match 17.0%; Score 45.5; DB 14; Length 44;
Best Local Similarity 52.2%; Pred. No. 2.9e+02;
Matches 12; Conservative 1; Mismatches 1; Indels 9; Gaps 2;

QY 4 RYGFQDPALYKE-----GDPAPY 21
Db 15 RYGWD----YKELAAARNGIPAPY 33

RESULT 16
US-10-477-525-15
; Sequence 15, Application US/10477525
; Publication No. US20050107314A1
; GENERAL INFORMATION:
; APPLICANT: GORCZYNSKI, Reginald M.
; APPLICANT: MARSDEN, Philip

; TITLE OF INVENTION: Modulation of CD200 Receptors
; FILE REFERENCE: 9579-81
; CURRENT APPLICATION NUMBER: US/10/477,525
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/292,950
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/369,862
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD200R1
; US-10-477-525-15

Query Match 16.8%; Score 45; DB 17; Length 24;
Best Local Similarity 39.3%; Pred. No. 1.7e+02;
Matches 11; Conservative 1; Mismatches 10; Indels 6; Gaps 1;

QY 20 PYKNPERWYRASFPITVTAAHSGTYRC 47
Db 3 PDHSPE-----LQISAVTLQHEGYTC 24

RESULT 17
US-10-040-862-10445
; Sequence 10445, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10445
; LENGTH: 30
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-040-862-10445

Query Match 16.8%; Score 45; DB 14; Length 30;
Best Local Similarity 53.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 35 ITVTAHSGTYRC 47
:::|||||
Db 4 LSLTAHSGNYSC 16

RESULT 18

US-10-057-475B-10445
; Sequence 10445, Application US/10057475B
; Publication No. US20040002068A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordonez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies

; FILE REFERENCE: 014058-014402US

; CURRENT APPLICATION NUMBER: US/10/057,475B

; CURRENT FILING DATE: 2002-01-22

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: US 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: US 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: US 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: US 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 60/222,903

; PRIOR FILING DATE: 2000-08-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 10979

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10445

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-057-475B-10445

Query Match 16.8%; Score 45; DB 15; Length 30;
Best Local Similarity 53.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 35 ITVTAHSGTYRC 47
:::|||||
Db 4 LSLTAHSGNYSC 16

RESULT 19

US-10-154-884B-10445

; Sequence 10445, Application US/10154884B

; Publication No. US20040005561A1

; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 11290

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10445

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-154-884B-10445

Query Match 16.8%; Score 45; DB 15; Length 30;
Best Local Similarity 53.8%; Pred. No. 2.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 35 ITVTAHSGTYRC 47
:::|||||
Db 4 LSLTAHSGNYSC 16

RESULT 20

US-10-764-324-10445

; Sequence 10445, Application US/10764324

; Publication No. US20040175739A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Retter, Marc

; APPLICANT: Corixa Corporation

; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies

; FILE REFERENCE: 014058-013520US

; CURRENT APPLICATION NUMBER: US/10/764,324

; CURRENT FILING DATE: 2004-01-23

; PRIOR APPLICATION NUMBER: US/10/040,862

; PRIOR FILING DATE: 2001-11-06

; PRIOR APPLICATION NUMBER: US 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: US 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: US 60/200,303


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RESULT 24
US-10-091-504-997
; Sequence 997, Application US/10091504
; Publication No. US20030059908A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C1
; CURRENT APPLICATION NUMBER: US/10/091,504
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 997
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-091-504-997

Query Match          16.6%; Score 44.5; DB 14; Length 45;
Best Local Similarity 38.5%; Pred. No. 4e+02;
Matches 15; Conservative 1; Mismatches 12; Indels 11; Gaps 2;

QY      9 QFALYKEGDPAPYKNPERWYRASFPFIITVTAHSGTYRC 47
      |||||
Db      1 QFLLDKLG-----MVTASIPLI--TGVHSGKNRC 28

RESULT 25
US-10-227-577-997
; Sequence 997, Application US/10227577
; Publication No. US20040005575A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C2
; CURRENT APPLICATION NUMBER: US/10/227,577
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/091,504
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 09/764,869
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 997
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (42)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 04:08:36 ; Search time 38 Seconds
(without alignments)
119.005 Million cell updates/sec

Title: US-09-503-387-3_COPY_134_180
Perfect score: 268
Sequence: 1 CQTRYGFDQFALYKEGDPAP.....YRASFPITVTAAHSGTYRC 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11254

Minimum DB seq length: 0
Maximum DB seq length: 48

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_79:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	37	13.8	29	S10061	Ig heavy chain (cl
2	36	13.4	43	B42057	fibroblast growth
3	36	13.4	47	A41266	fibroblast growth
4	35.5	13.2	34	S65716	prostaglandin-D sy
5	35	13.1	24	T42256	protein phosphatas
6	35	13.1	30	D70144	hypothetical prote
7	35	13.1	36	S07052	neuropeptide Y - s
8	35	13.1	38	PL0229	T-cell receptor be
9	35	13.1	46	D84334	hypothetical prote
10	34	12.7	20	T50757	pufk protein limpo
11	34	12.7	33	H81220	hypothetical prote
12	33	12.3	27	PN0586	tyrosine 3-monooxy
13	33	12.3	35	E38601	Ig kappa chain V r
14	33	12.3	35	AE0612	hypothetical prote
15	33	12.3	36	A28578	pancreatic hormone
16	33	12.3	38	G45095	photosystem I ligh
17	33	12.3	39	S00490	RNA-binding protei
18	33	12.3	44	F85701	hypothetical prote
19	33	12.3	44	G85701	hypothetical prote
20	32.5	12.1	31	T48290	hypothetical prote
21	32.5	12.1	38	S40096	chlorophyll a/b-bi
22	32.5	12.1	42	JE0021	probable 4.8K prot
23	32.5	12.1	44	AD1753	Lactococcus lactis
24	32.5	12.1	46	PC1066	antimorphine pepti
25	32	11.9	20	S18582	hypothetical prote
26	32	11.9	24	A60556	cytochrome c552 -
27	32	11.9	24	S35641	DNA (cytosine-5)-
28	32	11.9	30	S20778	Ig heavy chain V r
29	32	11.9	36	A30485	neuropeptide Y - r

30	32	11.9	36	2	B30485	neuropeptide Y - g
31	32	11.9	36	2	S00317	photosystem I 11K
32	32	11.9	41	2	G70214	hypothetical prote
33	32	11.9	42	2	S20767	Ig heavy chain V r
34	32	11.9	43	2	A43616	actin alpha, cardi
35	31.5	11.8	29	2	B81006	hypothetical prote
36	31.5	11.8	35	2	S13435	lectin III - furze
37	31	11.6	11	2	D61033	ranatathykinin D -
38	31	11.6	29	2	S58388	T-cell receptor be
39	31	11.6	30	2	S60336	phosphatidylinoit
40	31	11.6	31	2	T01701	hypothetical prote
41	31	11.6	34	2	S36843	defensin NP-6 - ra
42	31	11.6	34	2	F82163	hypothetical prote
43	31	11.6	36	1	NYPGY	neuropeptide Y - p
44	31	11.6	37	2	C83780	hypothetical prote
45	31	11.6	39	2	JT0620	glutamate dehydrog
46	31	11.6	39	2	S20769	Ig heavy chain V r
47	31	11.6	39	2	IS1219	adrenergic recepto
48	31	11.6	40	2	A40128	probable antigen 1
49	31	11.6	41	2	PQ0104	microbial serine p
50	31	11.6	46	2	B47187	phosphoprotein pho
51	31	11.6	47	2	JT0518	Ig heavy chain V-I
52	31	11.6	47	2	A81730	hypothetical prote
53	30.5	11.4	35	2	C44918	lactococcin G pept
54	30.5	11.4	40	2	S56006	tokaracetin alpha
55	30.5	11.4	40	2	T07560	hypothetical prote
56	30.5	11.4	41	2	B27579	T-cell receptor be
57	30.5	11.4	42	2	B82770	hypothetical prote
58	30.5	11.4	45	2	B97484	hypothetical prote
59	30	11.2	10	2	F49033	T-cell receptor ga
60	30	11.2	21	2	PQ0145	glucan endo-1,3-be
61	30	11.2	25	2	IS1151	alpha actin - quai
62	30	11.2	30	2	C32946	serine proteinase
63	30	11.2	33	2	PH1743	Ig heavy chain V r
64	30	11.2	35	2	I55263	alpha-smooth muscl
65	30	11.2	35	2	I64003	hypothetical prote
66	30	11.2	35	2	A85660	hypothetical prote
67	30	11.2	37	2	A36440	NADH2 peroxidase (
68	30	11.2	37	2	G82814	hypothetical prote
69	30	11.2	38	2	T01677	pseudo-kallikrein
70	30	11.2	38	2	B24376	trypsin inhibitor
71	30	11.2	38	2	A49040	T-cell receptor be
72	30	11.2	38	2	A44862	microtubule associ
73	30	11.2	41	2	F95098	hypothetical prote
74	30	11.2	45	1	RUDVD	rubredoxin [valida
75	30	11.2	46	2	AI0624	probable DNA inver
76	30	11.2	46	2	C83437	hypothetical prote
77	30	11.2	48	2	D83898	hypothetical prote
78	29	10.8	14	2	PH0792	T-cell receptor al
79	29	10.8	17	2	S57991	hydroxyproline-ric
80	29	10.8	18	2	A59137	protein Pil - gold
81	29	10.8	19	2	A41668	integrin alpha-7 c
82	29	10.8	20	2	A36045	thrombospondin hom
83	29	10.8	22	2	B32946	serine proteinase
84	29	10.8	24	2	S65714	lectin GNL alpha c
85	29	10.8	27	2	PH1720	Ig heavy chain V r
86	29	10.8	29	2	D32533	class II histocomp
87	29	10.8	30	2	H81202	hypothetical prote
88	29	10.8	32	2	PC4433	paired box transcr
89	29	10.8	33	2	PC4435	paired box transcr
90	29	10.8	34	2	PS0137	H-2 class I histoc
91	29	10.8	35	2	F84395	hypothetical prote
92	29	10.8	35	2	B41161	29K antigen PEB2 -
93	29	10.8	36	2	A39393	neuropeptide Y - l
94	29	10.8	36	2	A48540	neuropeptide Y - c
95	29	10.8	36	2	PN0041	actin 1 - mouse (f
96	29	10.8	37	2	B45875	Tla class I histoc
97	29	10.8	42	2	S29098	glutathione transf
98	29	10.8	43	2	B97155	hypothetical prote
99	29	10.8	45	2	S20776	Ig heavy chain V r
100	29	10.8	46	2	I39904	GTP cyclohydrolase

ALIGNMENTS

RESULT 1
S10061
Ig heavy chain (clone J12) - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 15-Oct-1999
C;Accession: S10061; E49021
R;Schwager, J.; Grossberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus laevis
A;Reference number: S01158; MUID:89052653; PMID:2903824
A;Accession: S10061
A;Molecule type: mRNA
A;Residues: 1-29 <SCH>
A;Cross-references: EMBL:X14925; NID:g64844; PIDN:CAA33052.1; PID:g930274
A;Note: the authors translated the codon AAG for residue 5 as Leu and GAG for residue 8
R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation
A;Reference number: A47624; MUID:90237760; PMID:2110243
A;Accession: E49021
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 10-24 <HAI>
A;Note: J8 region
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-24/Domain: V-D-J region (fragment) #status predicted <VRE>
F;25-29/Domain: C region (mu chain) (fragment) #status predicted <CRE>

Query Match 13.8%; Score 37; DB 2; Length 29;
Best Local Similarity 38.5%; Pred. No. 4.2e+02;
Matches 10; Conservative 5; Mismatches 9; Indels 2; Gaps 1;

QY 19 APYKNPERWYR--ASFPIITVTAHS 42
: ||| |||:: : |||: |||
Db 2 ARYKGVRYFEHWGQGTMTVTSATS 27
: ||| |||:: : |||: |||

RESULT 2
B42057
fibroblast growth factor receptor 1, membrane-bound - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B42057
R;Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
Mol. Cell. Biol. 12, 82-88, 1992
A;Title: Differential splicing in the extracellular region of fibroblast growth factor receptor 1
A;Reference number: A42057; MUID:92107200; PMID:1309595
A;Accession: B42057
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-43 <WER>
A;Cross-references: UNIPROT:Q9JUJ17; UNIPROT:Q9QZM7; GB:M80363
C;Keywords: growth factor receptor; membrane protein

Query Match 13.4%; Score 36; DB 2; Length 43;
Best Local Similarity 50.0%; Pred. No. 8.4e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 34 IITVTAHSGTYRC 47
: ||| ||| ||| |||
Db 13 LFNVTQAQSGEYVC 26
: ||| ||| ||| |||

RESULT 3
A41266
fibroblast growth factor receptor 1, membrane-bound - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
C;Accession: A41266

R;Johnson, D.E.; Lu, J.; Chen, H.; Werner, S.; Williams, L.T.
Mol. Cell. Biol. 11, 4627-4634, 1991
A;Title: The human fibroblast growth factor receptor genes: a common structural arrangement
A;Reference number: A41266; MUID:91342665; PMID:1652059
A;Accession: A41266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-47 <JOH>
A;Cross-references: UNIPROT:Q9UDF1
C;Keywords: growth factor receptor; membrane protein

Query Match 13.4%; Score 36; DB 2; Length 47;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 34 IITVTAHSGTYRC 47
: ||| ||| ||| |||
Db 14 LFNVTQAQSGEYVC 27
: ||| ||| ||| |||

RESULT 4
S65716
prostaglandin-D synthase (EC 5.3.99.2) - human (fragments)
N;Alternate names: prostaglandin-H2 D-isomerase
C;Species: Homo sapiens (man)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-May-1997
C;Accession: S65716
R;Giacomelli, S.; Leone, M.G.; Grima, J.; Silvestrini, B.; Cheng, C.Y.
Biochim. Biophys. Acta 1310, 269-276, 1996
A;Title: Astrocytes synthesize and secrete prostaglandin D synthetase in vitro.
A;Reference number: S65716; MUID:96177373; PMID:8599604
A;Accession: S65716
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16;17-34 <GIA>
C;Superfamily: lipocalin; lipocalin homology
C;Keywords: intramolecular oxidoreductase; isomerase

Query Match 13.2%; Score 35.5; DB 2; Length 34;
Best Local Similarity 46.7%; Pred. No. 7.6e+02;
Matches 7; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 7 FDQFA-LYKEGDPAP 20
: |||: |||: |||: |||
Db 19 YDQVALLYSGSKGP 33
: |||: |||: |||: |||

RESULT 5
T42256
protein phosphatase X - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42256
R;Zeke, T.; Gergely, P.; Dombradi, V.
submitted to the EMBL Data Library, July 1996
A;Description: The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabditis elegans
A;Reference number: Z22131
A;Accession: T42256
A;Status: preliminary; translated from GB/EMBL/DDDBJ
A;Molecule type: DNA
A;Residues: 1-24 <ZEK>
A;Cross-references: UNIPROT:Q94375; EMBL:Z77736; PIDN:CAB01295.1
C;Genetics:
A;Note: PPX
C;Superfamily: serine/threonine protein phosphatase; phosphoesterase core homology; phosphatase

Query Match 13.1%; Score 35; DB 2; Length 24;
Best Local Similarity 35.3%; Pred. No. 6.2e+02;
Matches 6; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 7 FDQFALYKEGDPAPYKN 23
: |||: |||: |||: |||
Db 3 YDLMELFRVGGPVPNTN 19
: |||: |||: |||: |||

RESULT 6
D70144
hypothetical protein B80357 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: D70144
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
son, D.; Peterson, J.; Karlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: D70144
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-30 <KLE>
A:Cross-references: UNIPROT:O51332; GB:AE001141; GB:AE000783; NID:g2688250; PIDN:AAC6673
A:Experimental source: strain B31

Query Match 13.1%; Score 35; DB 2; Length 30;
Best Local Similarity 42.9%; Pred. No. 7.8e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 21 YKNPERWYRASFPPI 34
| | | | | | | | | |
Db 8 YSKPDRFYFLGVPI 21

RESULT 7
S07052
neuropeptide Y - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S07052
R:Sillard, R.; Agerberth, B.; Mutt, V.; Joernvall, H.
FEBS Lett. 258, 263-265, 1989
A:Title: Sheep neuropeptide Y. A third structural type of a highly conserved peptide.
A:Reference number: S07052; MUID:90092485; PMID:2599092
A:Accession: S07052
A:Molecule type: protein
A:Residues: 1-36 <SIL>
A:Cross-references: UNIPROT:P14765
C:Function:
A:Description: neuropeptide inducing a number of behavioral effects including stimulation
C:Superfamily: pancreatic hormone
C:Keywords: amidated carboxyl end; appetite; hormone; neuropeptide
F;1-36/Product: neuropeptide Y #status experimental <MAT>
F;36/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 13.1%; Score 35; DB 2; Length 36;
Best Local Similarity 46.7%; Pred. No. 9.4e+02;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 16 GDPAPYKNPERWYRA 30
| | | | | | | | | |
Db 9 GDDAPAEADLARYISA 23

RESULT 8
PL0229
T-cell receptor beta chain V region (V-beta-6.7a, PCR-2) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 30-May-1997
C:Accession: PL0229
R:Li, Y.; Szabo, P.; Robinson, M.A.; Dong, B.; Posnett, D.N.
J. Exp. Med. 171, 221-230, 1990
A:Title: Allelic variations in the human T cell receptor V-beta-6.7 gene products.
A:Reference number: PL0225; MUID:90111615; PMID:1967299
A:Accession: PL0229
A:Molecule type: mRNA

A:Residues: 1-38 <LIY>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 13.1%; Score 35; DB 2; Length 38;
Best Local Similarity 40.0%; Pred. No. 9.9e+02;
Matches 6; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 9 QFALYKEGDPAPYKN 23
| | | | | | | | | |
Db 23 EFLIYFQGNAPDKS 37

RESULT 9
D84334
hypothetical protein Vng1832h [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: D84334
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: D84334
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-46 <STO>
A:Cross-references: UNIPROT:Q9HP30; GB:AE004437; NID:g10581278; PIDN:AAG20040.1; GSPDB:G
C:Genetics:
A:Gene: VNG1832H

Query Match 13.1%; Score 35; DB 2; Length 46;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 18 PAPYKNPERWYRAS 31
| | | | | | | | | |
Db 12 PAAIRNDTRGYRSS 25

RESULT 10
T50757
pufK protein [imported] - Rhodobacter sphaeroides
C:Species: Rhodobacter sphaeroides
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C:Accession: T50757
R:Choudhary, M.; Kaplan, S.
Nucleic Acids Res. 28, 862-867, 2000
A:Title: DNA sequence analysis of the photosynthesis region of Rhodobacter sphaeroides 2
A:Reference number: Z25222; MUID:20115911; PMID:10648776
A:Accession: T50757
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-20 <CHO>
A:Cross-references: UNIPROT:Q53121; EMBL:AF195122; PIDN:AAF24301.1
A:Experimental source: strain 2.4.1
C:Genetics:
A:Gene: pufK

Query Match 12.7%; Score 34; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 20 PYKNPERWYRAS 31
| | | | | | | | | |
Db 3 PYRNPRHQHVAS 14

RESULT 11
H81220

hypothetical protein NMB0233 [imported] - Neisseria meningitidis (strain MC58 serogroup C); Species: Neisseria meningitidis
C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C; Accession: H81220
R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A; Reference number: A81000; MUID:20175755; PMID:10710307
A; Accession: H81220
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-33 <RET>
A; Cross-references: UNIPROT:Q9K1C9; GB:AE002381; GB:AE002098; NID:g7225455; PIDN:AAF4068
A; Experimental source: serogroup B, strain MC58
C; Genetics:
A; Gene: NMB0233

	Query Match	12.7%	Score 34;	DB 2;	Length 33;
Best Local Similarity	28.0%;	Pred. No. 1.1e+03;			
Matches	7;	Conservative 6;	Mismatches 12;	Indels 0;	Gaps 0;

QY 21 YKNPERWYRASFPITVTAAHSCTY 45
|:: :: | : | ||: |
Db 5 YESPKFQTAFIAVIIVDEAHATMY 29

RESULT 12
PN0586
tyrosine 3-monooxygenase (EC 1.14.16.2) type 3 and 4 - common gibbon (fragment)
N; Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase
C; Species: Hylobates lar (common gibbon, white-handed gibbon)
C; Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C; Accession: PN0586
R; Ichinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
Biochem. Biophys. Res. Commun. 195, 158-165, 1993
A; Title: Increased heterogeneity of tyrosine hydroxylase in humans.
A; Reference number: PN0575; MUID:93371398; PMID:7689834
A; Accession: PN0586
A; Molecule type: genomic RNA
A; Residues: 1-27 <ICH>
A; Cross-references: UNIPROT:Q7M344; GB:L14793
A; Experimental source: lymph nodes
C; Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosynthesis
C; Superfamily: phenylalanine 4-monooxygenase
C; Keywords: bioppterin; monooxygenase; oxidoreductase

	Query Match	12.3%	Score 33;	DB 2;	Length 27;
Best Local Similarity	30.4%;	Pred. No. 1.2e+03;			
Matches	7;	Conservative 2;	Mismatches 14;	Indels 0;	Gaps 0;

QY 16 GDPAPYKNPERWYRASFPITVT 38
||| | | : | : |
Db 1 GDPGSLTGSPPWPCTAAPASYT 23

RESULT 13
E38601
Ig kappa chain V region (I4D2) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 23-Jul-1999
C; Accession: E38601
R; Goshorn, S.C.; Retzel, E.; Jermerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A; Title: Common structural features among monoclonal antibodies binding the same antigen
A; Reference number: A38601; MUID:91115823; PMID:1703527
A; Accession: E38601
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-35 <GOS>
A; Cross-references: GB:M57982; NID:g196410; PIDN:AAA63363.1; PID:g196411

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 12.3%; Score 33; DB 2; Length 35;
Best Local Similarity 41.2%; Pred. No. 1.6e+03;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 31 SFPIITVTAHSGTYRC 47
 | :| :|||
Db 6 SLTISMEADAATYYC 22

RESULT 14
AE0612
hypothetical protein STY0965 [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
R;Accession: AE0612
C;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.H.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium DT104
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AE0612
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-35 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD05367.1; PID:g16502131; GSPDB:GN00176
C;Genetics:
A;Gene: STY0965

Query Match 12.3%; Score 33; DB 2; Length 35;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 9; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

Qy 2 QTRYGFD--QFALYKEGDPAFYKNPNER 26
 |||||-----|||
Db 2 QAIFYAFRRQRKEYNRGGEGAYKSIEK 28

RESULT 15
A28578
pancreatic hormone - ostrich
N;Alternate names: pancreatic polypeptide
C;Species: Struthio camelus (ostrich)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C;Accession: A28578
R;Litthauer, D.; Oelofsen, W.
Int. J. Pept. Protein Res. 29, 739-745, 1987
A;Title: Purification and primary structure of ostrich pancreatic polypeptide.
A;Reference number: A28578; MUID:87307111; PMID:3623804
A;Accession: A28578
A:Molecule type: protein
A;Residues: 1-36 <LIT>
A;Cross-references: UNIPROT:P11967
A;Note: the sequence of residues 22-23 was reported as Asn-Asp in Fig. 7 and as Asp-Asn in Fig. 8
C;Superfamily: pancreatic hormone

Query Match 12.3%; Score 33; DB 2; Length 36;
Best Local Similarity 30.8%; Pred. No. 1.7e+03;
Matches 8; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 16 GDPAPYKNPERWYRASFPFIITVTAAH 41
 ||||:|:|
Db 9 GDPAVEDLVRFYDNLQQYLNVVTRH 34

RESULT 16
G45095
photosystem I light-harvesting complex chlorophyll a/b protein p22.1/p22 - Chlamydomonas reinhardtii

```

Best Local Similarity 36.4%; Pred. No. 2.1e+03;
Matches 8; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 27 WYRASFPPIIT--VTAHSGTYR 46
Db 20 WHDLAAPILAGIITAAIVGWR 41
      | : ||| : ||| | : |
      | : ||| : ||| | : |

RESULT 19
G85701
hypothetical protein Z1989 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: G85701
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85701
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-44 <SFO>
A;Cross-references: UNIPROT:Q9X4I5; GB:AE005174; NID:G12514933; PIDN:AAG56075.1; GSPDB:G1
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1989

Query Match 12.3%; Score 33; DB 2; Length 44;
Best Local Similarity 36.4%; Pred. No. 2.1e+03;
Matches 8; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 27 WYRASFPPIIT--VTAHSGTYR 46
Db 20 WHDLAAPILAGIITAAIVGWR 41
      | : ||| : ||| | : |
      | : ||| : ||| | : |

RESULT 20
T48290
hypothetical protein T22P11.280 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48290
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24490
A;Accession: T48290
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-31 <BEV>
A;Cross-references: UNIPROT:Q9LZ33; EMBL:AL162971
A;Experimental source: cultivar Columbia; BAC clone T22P11
C;Genetics:
A;Map position: 5
A;Introns: 26/2
A;Note: T22P11.280

Query Match 12.1%; Score 32.5; DB 2; Length 31;
Best Local Similarity 34.8%; Pred. No. 1.7e+03;
Matches 8; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

QY 10 FALYKEGDDPA-PYKNPERWYRAS 31
Db 8 FKQSKDDSSGSGFKTKELWYLSS 30
      | | : : | : | | : |
      | | : : | : | | : |

RESULT 21
S40096
chlorophyll a/b-binding protein - moss (Physcomitrella patens)
C;Species: Physcomitrella patens
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S40096
R;Reeki, R.; Faust, M.; Wang, X.H.; Wehe, M.; Abel, W.O.

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 04:16:51 ; Search time 174 Seconds
(without alignments)
138.320 Million cell updates/sec

Title: US-09-503-387-3_COPY_134_180
Perfect score: 268
Sequence: 1 CQTRVGFQFALYKEGDPAP.....YRASFPITVTAHSGTYRC 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 64033

Minimum DB seq length: 0
Maximum DB seq length: 48

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	16.4	48	Q8AFG1	Q8afg1 mouse mamma
2	42	15.7	40	Q8EZ89	Q8ez89 leptospira
3	41	15.3	25	Q93LX3	Q93lx3 vibrio chol
4	41	15.3	35	Q8LRV5	Q8lrsv bacillus an
5	41	15.3	42	Q7R533	Q7r533 giardia lam
6	41	15.3	47	Q70U90	Q70u90 mycena pura
7	39	14.6	20	Q8NFW3	Q8nfw3 homo sapien
8	39	14.6	32	Q8UUN6	Q8uun6 xenopus lae
9	39	14.6	33	Q24624	Q24624 pinus taeda
10	39	14.6	39	Q9HF16	Q9hfl6 epichloe am
11	39	14.6	39	Q9HF17	Q9hfl7 epichloe cf
12	39	14.6	41	Q8JLH0	Q8jllh0 cryphonectr
13	39	14.6	46	Q80BI8	Q80bi8 saimirine
14	39	14.6	46	Q80BJ4	Q80bj4 saimirine
15	39	14.6	46	Q80BR5	Q80br5 saimirine
16	39	14.6	46	Q80BR5	Q80br5 saimirine
17	39	14.6	47	Q6V8T8	Q6v8t8 malus domes
18	38.5	14.4	40	Q6U847	Q6u847 mycobacteri
19	38	14.2	28	Q7G1I0	Q7g1i0 pinus taeda
20	38	14.2	32	Q96WI2	Q96wi2 neotyphodiu
21	38	14.2	33	Q24637	Q24637 pinus taeda
22	38	14.2	39	Q7LTM6	Q7ltm6 epichloe ty
23	38	14.2	39	Q7LTM7	Q7ltm7 epichloe ty
24	38	14.2	39	Q7LTM8	Q7ltm8 epichloe ty
25	38	14.2	39	Q7LTM9	Q7ltm9 epichloe ty
26	38	14.2	39	Q7LTN0	Q7ltn0 epichloe ty
27	38	14.2	39	Q7LTN1	Q7ltn1 epichloe ty
28	38	14.2	39	Q7LTN2	Q7ltn2 epichloe ty
29	38	14.2	39	Q7LTN3	Q7ltn3 epichloe ty
30	38	14.2	39	Q7LTN4	Q7ltn4 epichloe ty
31	38	14.2	39	Q7LTN5	Q7ltn5 epichloe ty

32	38	14.2	39	2	Q7LTM6	Q7ltn6 epichloe sy
33	38	14.2	39	2	Q7LTM7	Q7ltn7 epichloe gl
34	38	14.2	39	2	Q7LTM8	Q7ltn8 epichloe fe
35	38	14.2	39	2	Q7LTM9	Q7ltn9 epichloe fe
36	38	14.2	39	2	Q7LTP0	Q7ltp0 epichloe el
37	38	14.2	39	2	Q7LTP1	Q7ltp1 epichloe el
38	38	14.2	39	2	Q7LTP2	Q7ltp2 epichloe el
39	38	14.2	39	2	Q7LTP3	Q7ltp3 epichloe br
40	38	14.2	39	2	Q7LTP4	Q7ltp4 epichloe br
41	38	14.2	39	2	Q7LTP5	Q7ltp5 epichloe br
42	38	14.2	39	2	Q7LTP6	Q7ltp6 epichloe br
43	38	14.2	39	2	Q7LTP7	Q7ltp7 epichloe ba
44	38	14.2	39	2	Q9HDM2	Q9hdm2 epichloe ba
45	38	14.2	39	2	Q9HDM3	Q9hdm3 epichloe br
46	38	14.2	39	2	Q9HDM4	Q9hdm4 epichloe br
47	38	14.2	39	2	Q9HDM5	Q9hdm5 epichloe el
48	38	14.2	39	2	Q9HDM6	Q9hdm6 epichloe fe
49	38	14.2	39	2	Q9HDM7	Q9hdm7 epichloe gl
50	38	14.2	39	2	Q9HDM8	Q9hdm8 epichloe sy
51	38	14.2	39	2	Q9HDM9	Q9hdm9 epichloe ty
52	38	14.2	39	2	Q9HF13	Q9hfl3 epichloe ty
53	38	14.2	39	2	Q9HF14	Q9hfl4 epichloe cl
54	38	14.2	40	2	Q72F30	Q72f30 desulfovibr
55	38	14.2	45	2	Q95V78	Q95v78 bombyx mori
56	37.5	14.0	39	2	Q13254	Q13254 homo sapien
57	37	13.8	20	2	Q8X127	Q8x127 magnaporthe
58	37	13.8	20	2	Q8X128	Q8x128 magnaporthe
59	37	13.8	20	2	Q96VW9	Q96vw9 magnaporthe
60	37	13.8	20	2	Q96VW0	Q96vw0 magnaporthe
61	37	13.8	20	2	Q96VW1	Q96vw1 magnaporthe
62	37	13.8	20	2	Q96VW2	Q96vw2 magnaporthe
63	37	13.8	20	2	Q9C2Z3	Q9c2z3 sclerotinia
64	37	13.8	20	2	Q9C2Z4	Q9c2z4 sclerotinia
65	37	13.8	20	2	Q9C2Z5	Q9c2z5 sclerotinia
66	37	13.8	20	2	Q9C2Z6	Q9c2z6 sclerotinia
67	37	13.8	20	2	Q9C2Z7	Q9c2z7 sclerotinia
68	37	13.8	20	2	Q9C2Z8	Q9c2z8 sclerotinia
69	37	13.8	20	2	Q9C2Z9	Q9c2z9 sclerotinia
70	37	13.8	20	2	Q9C300	Q9c300 sclerotinia
71	37	13.8	20	2	Q9C301	Q9c301 sclerotinia
72	37	13.8	20	2	Q9C302	Q9c302 sclerotinia
73	37	13.8	20	2	Q9C303	Q9c303 sclerotinia
74	37	13.8	20	2	Q9C304	Q9c304 sclerotinia
75	37	13.8	20	2	Q9C305	Q9c305 sclerotinia
76	37	13.8	20	2	Q9C306	Q9c306 sclerotinia
77	37	13.8	20	2	Q9C307	Q9c307 sclerotinia
78	37	13.8	20	2	Q9C308	Q9c308 sclerotinia
79	37	13.8	20	2	Q9C309	Q9c309 sclerotinia
80	37	13.8	20	2	Q9C310	Q9c310 sclerotinia
81	37	13.8	20	2	Q9C311	Q9c311 sclerotinia
82	37	13.8	20	2	Q9C312	Q9c312 sclerotinia
83	37	13.8	20	2	Q9C313	Q9c313 sclerotinia
84	37	13.8	20	2	Q9C314	Q9c314 sclerotinia
85	37	13.8	20	2	Q9C315	Q9c315 sclerotinia
86	37	13.8	20	2	Q9C316	Q9c316 sclerotinia
87	37	13.8	20	2	Q9C317	Q9c317 sclerotinia
88	37	13.8	20	2	Q9C318	Q9c318 sclerotinia
89	37	13.8	20	2	Q9C319	Q9c319 sclerotinia
90	37	13.8	20	2	Q9C320	Q9c320 sclerotinia
91	37	13.8	20	2	Q9C321	Q9c321 sclerotinia
92	37	13.8	20	2	Q9C322	Q9c322 sclerotinia
93	37	13.8	20	2	Q9C323	Q9c323 sclerotinia
94	37	13.8	20	2	Q9C324	Q9c324 sclerotinia
95	37	13.8	20	2	Q9C325	Q9c325 sclerotinia
96	37	13.8	20	2	Q9C326	Q9c326 sclerotinia
97	37	13.8	20	2	Q9C327	Q9c327 sclerotinia
98	37	13.8	20	2	Q9C328	Q9c328 sclerotinia
99	37	13.8	20	2	Q9C329	Q9c329 sclerotinia
100	37	13.8	20	2	Q9C330	Q9c330 sclerotinia

ALIGNMENTS


```
RESULT 1
Q8AFG1      PRELIMINARY;      PRT;      48 AA.
AC  Q8AFG1;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Envelope polyprotein (Fragment).
OS  Mouse mammary tumor virus.
OC  Viruses; Retroid viruses; Retroviridae; Betaretrovirus;
OC  Mammalian type B retroviruses.
OX  NCBI_TaxID=11757;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=10016;
RA  Polesz B.J., Perzova R.N., Abbott L.Z.;
RL  Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY152723; AAN7719.1; -.
DR  GO; GO:0019031; C:viral envelope; IEA.
KW  Envelope protein; Polyprotein.
FT  NON TER      1
FT  NON TER      48
SQ  SEQUENCE 48 AA; 5402 MW; 67028A527E8DF382 CRC64;
```

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Query Match      16.4%; Score 44; DB 2; Length 48;
Best Local Similarity 36.4%; Pred. No. 3.9e+02;
Matches 12; Conservative 3; Mismatches 12; Indels 6; Gaps 2;
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Qy  1 CQTRYGFQFALYKEGDPAPYKNPERMYRASFP 33
    ||: || ||| : ||| : ||| : ||
Db  11 CQIAFKKDAF---WEGDESA---PPRWLPCAF 37
```

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RESULT 2
Q8EZ89      PRELIMINARY;      PRT;      40 AA.
AC  Q8EZ89;
DT  01-MAR-2003 (TrEMBLrel. 23, Created)
DT  01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT  01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE  Hypothetical protein.
GN  OrderedLocusNames=LA3967;
OS  Leptospira interrogans.
OC  Bacteria; Spirochaetes; Spirochaetales; Leptospiaceae; Leptospira.
OX  NCBI_TaxID=173;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
RX  MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA  Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA  Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA  Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA  Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA  Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
RA  Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA  Xu J.-G., Zhao G.-P.;
RT  "Unique physiological and pathogenic features of Leptospira
RT  interrogans revealed by whole-genome sequencing.";
RL  Nature 422:888-893(2003).
DR  EMBL; AE011552; AAN51165.1; -.
KW  Complete proteome.
SQ  SEQUENCE 40 AA; 5101 MW; C86960B8FEB3504A CRC64;
```

```
Query Match      15.7%; Score 42; DB 2; Length 40;
Best Local Similarity 50.0%; Pred. No. 5.8e+02;
Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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Qy  9 QFALYKEGDPAPYKNP 24
    ||: ||| | : ||
Db  22 QFSLYKNGRLLKQFANP 37
```

```
RESULT 3
Q93LX3      PRELIMINARY;      PRT;      25 AA.
AC  Q93LX3;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  Gida (Fragment).
GN  Name=gida;
OS  Vibrio cholerae.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC  Vibrionaceae; Vibrio.
OX  NCBI_TaxID=666;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=O395;
RA  Saha A., Haralalka S., Bhadra R.K.;
RL  Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=SG24;
RA  Saha A., Haralalka S., Bhadra R.K.;
RL  Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY034431; AAK61371.1; -.
DR  EMBL; AY211526; AAO53342.1; -.
FT  NON TER      25
SQ  SEQUENCE 25 AA; 2530 MW; F1EA964A47D01EE8 CRC64;
```

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Query Match      15.3%; Score 41; DB 2; Length 25;
Best Local Similarity 41.2%; Pred. No. 4.7e+02;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
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Qy  28 YRASFPIITVTAHSGT 44
    | : | : | : | : |
Db  3 YHETFDVIVVGGGHAGT 19
```

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RESULT 4
Q81RV5      PRELIMINARY;      PRT;      35 AA.
AC  Q81RV5; Q6KJ97;
DT  01-JUN-2003 (TrEMBLrel. 24, Created)
DT  01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT  25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE  Hypothetical protein.
GN  OrderedLocusNames=BA1932, GBAA1932;
OS  Bacillus anthracis.
OC  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX  NCBI_TaxID=1392;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Ames / isolate Porton;
RX  MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA  Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA  Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA  Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA  Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA  DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA  Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA  Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA  Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA  Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA  Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
RA  Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT  "The genome sequence of Bacillus anthracis Ames and comparison to
RT  closely related bacteria.";
RL  Nature 423:81-86(2003).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Ames / isolate 0581;
RA  Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA  Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA  Fraser C.M.;
```



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RL Sydowia 54:98-117(2002).
DR EMBL; AF368348; AAM20836.2; -.
FT NON_TER 1
FT NON_TER 41
SQ SEQUENCE 41 AA; 4579 MW; 4409FA444FD8C985 CRC64;

Query Match      14.6%; Score 39; DB 2; Length 41;
Best Local Similarity 28.6%; Pred. No. 1.5e+03;
Matches 6; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 20 PYKNPERWYRASFPIITVTAA 40
Db 17 PPPSPDFWHRRTFLFLPTSS 37

RESULT 13
Q80BJ8
ID Q80BI8 PRELIMINARY; PRT; 46 AA.
AC Q80BI8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6045;
RX MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
RA Ensser A., Thureau M., Wittmann S., Fickenscher H.;
RT "The genome of herpesvirus saimiri C488 which is capable of
transforming human T cells.";
RL Virology 314:471-487(2003).
DR EMBL; AJ410485; CAC85013.1; -.
KW Hypothetical protein.
FT NON_TER 46
SQ SEQUENCE 46 AA; 5325 MW; C5EDBFA59871761E CRC64;

Query Match      14.6%; Score 39; DB 2; Length 46;
Best Local Similarity 70.0%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 20 PYKNPERWYR 29
Db 2 PYKVPEIYYR 11

RESULT 14
Q80BJ4
ID Q80BJ4 PRELIMINARY; PRT; 46 AA.
AC Q80BJ4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A6051;
RX MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
RA Ensser A., Thureau M., Wittmann S., Fickenscher H.;
RT "The genome of herpesvirus saimiri C488 which is capable of
transforming human T cells.";
RL Virology 314:471-487(2003).
DR EMBL; AJ410483; CAC85007.1; -.
KW Hypothetical protein.
FT NON_TER 46
SQ SEQUENCE 46 AA; 5325 MW; C5EDBFA59871761E CRC64;
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Query Match      14.6%; Score 39; DB 2; Length 46;
Best Local Similarity 70.0%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 20 PYKNPERWYR 29
Db 2 PYKVPEIYYR 11

RESULT 15
Q80BJ7
ID Q80BJ7 PRELIMINARY; PRT; 46 AA.
AC Q80BJ7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A5747;
RX MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
RA Ensser A., Thureau M., Wittmann S., Fickenscher H.;
RT "The genome of herpesvirus saimiri C488 which is capable of
transforming human T cells.";
RL Virology 314:471-487(2003).
DR EMBL; AJ410482; CAC85001.1; -.
KW Hypothetical protein.
FT NON_TER 46
SQ SEQUENCE 46 AA; 5325 MW; C5EDBFA59871761E CRC64;

Query Match      14.6%; Score 39; DB 2; Length 46;
Best Local Similarity 70.0%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 20 PYKNPERWYR 29
Db 2 PYKVPEIYYR 11

RESULT 16
Q80BR5
ID Q80BR5 PRELIMINARY; PRT; 46 AA.
AC Q80BR5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
OS Saimiriine herpesvirus 2.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=10381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A6355;
RX MEDLINE=22918177; PubMed=14554077; DOI=10.1016/S0042-6822(03)00449-5;
RA Ensser A., Thureau M., Wittmann S., Fickenscher H.;
RT "The genome of herpesvirus saimiri C488 which is capable of
transforming human T cells.";
RL Virology 314:471-487(2003).
DR EMBL; AJ410484; CAC84287.1; -.
KW Hypothetical protein.
FT NON_TER 46
SQ SEQUENCE 46 AA; 5325 MW; C5EDBFA59871761E CRC64;

Query Match      14.6%; Score 39; DB 2; Length 46;
Best Local Similarity 70.0%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Best Local Similarity 39.3%; Pred. No. 1.5e+03; Matches 11; Conservative 0; Mismatches 9; Indels 8; Gaps 1;

QY 16 GDPAPYKNPERWYRASFPPIITVTAHSG 43
Db 13 GDDAP-----RAVFPISVGRPRHQ 32

RESULT 21
O24637
ID O24637 PRELIMINARY; PRT; 33 AA.
AC O24637;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NADPH:protochlorophyllide oxidoreductase porB (Fragment).
GN Name=porB-II; Synonyms=porB-I;
OS Pinus taeda (Loblolly pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3352;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RX MEDLINE=99003724; PubMed=9787456;
RA Skinner J.S., Timko M.P.;
RT "Loblolly pine (Pinus taeda L.) contains multiple expressed genes encoding light-dependent NADPH:protochlorophyllide oxidoreductase (POR).";
RL Plant Cell Physiol. 39:795-806(1998).
DR EMBL; AF027345; AAB86723.1; -.
DR EMBL; AF027338; AAB86716.1; -.
DR EMBL; AF027339; AAB86717.1; -.
DR EMBL; AF027340; AAB86718.1; -.
DR EMBL; AF027341; AAB86719.1; -.
DR EMBL; AF027343; AAB86721.1; -.
DR EMBL; AF027344; AAB86722.1; -.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR002197; HTH_Fis.
DR PRINTS; PR01590; HTHFIS.
FT NON_TER 33
SQ SEQUENCE 33 AA; 3331 MW; 4B781255B3F3DDAB CRC64;

Query Match 14.2%; Score 38; DB 2; Length 33;
Best Local Similarity 60.0%; Pred. No. 1.5e+03;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 QTRYGFDQFALYKEG 16
Db 6 QTHIGSVAFAQKEG 20

RESULT 22
Q7LTM6
ID Q7LTM6 PRELIMINARY; PRT; 39 AA.
AC Q7LTM6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Actin (Fragment).
GN Name=act1;
OS Epichloe typhina.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Epichloe.
OX NCBI_TaxID=5113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC201667;
RA Craven K.D., Hsiau P.T.W., Leuchtmann A., Hollin W., Schardl C.L.;
RT "Multigene phylogeny of Epichloe species, fungal symbionts of grasses.";
RL Ann. Mo. Bot. Gard. 88:14-34(2001).

DR EMBL; AF240114; AAG39722.1; -.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 3967 MW; 2C7E3265EA20F58C CRC64;

Query Match 14.2%; Score 38; DB 2; Length 39;
Best Local Similarity 39.3%; Pred. No. 1.9e+03;
Matches 11; Conservative 0; Mismatches 9; Indels 8; Gaps 1;

QY 16 GDPAPYKNPERWYRASFPPIITVTAHSG 43
Db 20 GDDAP-----RAVFPISVGRPRHQ 39

RESULT 23
Q7LTM7
ID Q7LTM7 PRELIMINARY; PRT; 39 AA.
AC Q7LTM7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Actin (Fragment).
GN Name=act1;
OS Epichloe typhina.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Epichloe.
OX NCBI_TaxID=5113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC201666;
RA Craven K.D., Hsiau P.T.W., Leuchtmann A., Hollin W., Schardl C.L.;
RT "Multigene phylogeny of Epichloe species, fungal symbionts of grasses.";
RL Ann. Mo. Bot. Gard. 88:14-34(2001).
DR EMBL; AF240113; AAG39721.1; -.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 3967 MW; 2C7E3265EA20F58C CRC64;

Query Match 14.2%; Score 38; DB 2; Length 39;
Best Local Similarity 39.3%; Pred. No. 1.9e+03;
Matches 11; Conservative 0; Mismatches 9; Indels 8; Gaps 1;

QY 16 GDPAPYKNPERWYRASFPPIITVTAHSG 43
Db 20 GDDAP-----RAVFPISVGRPRHQ 39

RESULT 24
Q7LTM8
ID Q7LTM8 PRELIMINARY; PRT; 39 AA.
AC Q7LTM8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Actin (Fragment).
GN Name=act1;
OS Epichloe typhina.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Epichloe.
OX NCBI_TaxID=5113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E348;
RA Craven K.D., Hsiau P.T.W., Leuchtmann A., Hollin W., Schardl C.L.;
RT "Multigene phylogeny of Epichloe species, fungal symbionts of grasses.";
RL Ann. Mo. Bot. Gard. 88:14-34(2001).
DR EMBL; AF240112; AAG39720.1; -.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 3967 MW; 2C7E3265EA20F58C CRC64;

Query Match 14.2%; Score 38; DB 2; Length 39;
Best Local Similarity 39.3%; Pred. No. 1.9e+03;
Matches 11; Conservative 0; Mismatches 9; Indels 8; Gaps 1;

QY 16 GDPAPYKNPERWYRASFPFIITVTAHSG 43
|||
Db 20 GDDAP-----RAVFPISIVGRPRHQG 39

RESULT 25

Q7LTM9 PRELIMINARY; PRT; 39 AA.
AC Q7LTM9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Actin (Fragment).
GN Name=act1;
OS Epichloe typhina.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Epichloe.
OX NCBI_TaxID=5113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC200851;
RA Craven K.D., Hsiau P.T.W., Leuchtmann A., Hollin W., Schardl C.L.;
RT "Multigene phylogeny of Epichloe species, fungal symbionts of
grasses.";
RL Ann. Mo. Bot. Gard. 88:14-34(2001).
DR EMBL; AF240111; AAG39719.1; -.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 3967 MW; 2C7E3265EA20F58C CRC64;

Query Match 14.2%; Score 38; DB 2; Length 39;
Best Local Similarity 39.3%; Pred. No. 1.9e+03;
Matches 11; Conservative 0; Mismatches 9; Indels 8; Gaps 1;

QY 16 GDPAPYKNPERWYRASFPFIITVTAHSG 43
|||
Db 20 GDDAP-----RAVFPISIVGRPRHQG 39

Search completed: October 29, 2005, 04:27:50
Job time : 178 secs